

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:18:17 ; Search time 127.5 Seconds  
(without alignments)  
99.280 Million cell updates/sec

Title: US-10-612-818-4

Perfect score: 125

Sequence: 1 RDGNPYAVCDKCLKFYISKISEY 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 02.4

1: uniprot\_sprot.4

2: uniprot\_trembl.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	81	2 Q80886	Q80886 human papil
2	125	100.0	84	2 Q80882	Q80882 human papil
3	125	100.0	90	2 Q80884	Q80884 human papil
4	125	100.0	90	2 Q80885	Q80885 human papil
5	125	100.0	91	2 Q80887	Q80887 human papil
6	125	100.0	99	2 Q91982	Q91982 human papil
7	125	100.0	103	2 Q91986	Q91986 human papil
8	125	100.0	130	2 Q91984	Q91984 human papil
9	125	100.0	130	2 Q91988	Q91988 human papil
10	125	100.0	130	2 Q91980	Q91980 human papil
11	125	100.0	130	2 Q91982	Q91982 human papil
12	125	100.0	130	2 Q91988	Q91988 human papil
13	125	100.0	130	2 Q91980	Q91980 human papil
14	125	100.0	138	2 Q91982	Q91982 human papil
15	125	100.0	143	2 Q91986	Q91986 human papil
16	125	100.0	143	2 Q91984	Q91984 human papil
17	125	100.0	151	2 Q12335	Q12335 human papil
18	125	100.0	151	2 Q12336	Q12336 human papil
19	125	100.0	151	2 Q76T50	Q76T50 human papil
20	125	100.0	151	2 Q77816	Q77816 human papil
21	125	100.0	151	2 Q77816	Q77816 human papil
22	125	100.0	151	2 Q77J57	Q77J57 human papil
23	125	100.0	151	2 Q77J55	Q77J55 human papil
24	125	100.0	151	2 Q80966	Q80966 human papil
25	125	100.0	151	2 Q89640	Q89640 human papil
26	125	100.0	151	2 Q89648	Q89648 human papil
27	125	100.0	151	2 Q89708	Q89708 human papil
28	125	100.0	151	2 Q89755	Q89755 human papil
29	125	100.0	151	2 Q89882	Q89882 human papil
30	125	100.0	151	2 Q89887	Q89887 human papil
31	125	100.0	151	2 Q8B564	Q8B564 human papil

32	125	100.0	151	2 Q8BB19	Q8BB19 human papil
33	125	100.0	151	2 Q8BB20	Q8BB20 human papil
34	125	100.0	151	2 Q8BB21	Q8BB21 human papil
35	125	100.0	151	2 Q8W8C3	Q8W8C3 human papil
36	125	100.0	151	2 Q8W931	Q8W931 human papil
37	125	100.0	151	2 Q8W9P2	Q8W9P2 human papil
38	125	100.0	151	2 Q8W9P4	Q8W9P4 human papil
39	125	100.0	151	2 Q8W9P5	Q8W9P5 human papil
40	125	100.0	151	1 V56 HPV16	P03126 human papil
41	125	100.0	158	2 Q71B17	Q71B17 human papil
42	125	100.0	158	2 Q8JMU8	Q8JMU8 human papil
43	125	100.0	158	2 Q8WH13	Q8WH13 human papil
44	125	100.0	158	2 Q8QDH3	Q8QDH3 human papil
45	125	100.0	158	2 Q8QDH9	Q8QDH9 human papil

## ALIGNMENTS

RESULT 1  
Q80886 PRELIMINARY; PRT; 81 AA.  
AC Q80886;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16; TISSUE=Cervical tissue;  
RA Haegert D.G., Galutira D.F., Younghusband B.H.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U14515; AAB60569.2;  
DR GO: GO:0042025; C:host cell nucleus; IEA.  
DR GO: GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON\_TER 1  
FT NON\_TER 81  
SQ SEQUENCE 81 AA; 9784 MW; DD5FEDBC9F845B97 CRC64;  
Query Match 100.0%; Score 125; DB 2; Length 81;  
Best Local Similarity 100.0%; Pred.No. 6.3e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
DB 14 RDGNPYAVCDKCLKFYISKISEY 35  
RESULT 2  
Q80882 PRELIMINARY; PRT; 84 AA.  
AC Q80882;  
DT 01-NOV-1996 (TRENBLrel. 01, Created)  
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16; TISSUE=Cervical;  
RA Haegert D.G., Galutira D.F., Younghusband B.H.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U14511; AAB60565.2;  
DR GO: GO:0042025; C:host cell nucleus; IEA.

DR GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 84 AA; 10177 MW; 5AB6B896468E1CAA CRC64;

Query Match 100.0%; Score 125; DB 2; Length 84;  
Best Local Similarity 100.0%; Pred. No. 6.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
DB 11 RDGNPYAVCDKCLKFYISKISEY 32

## RESULT 3

Q80884 ID Q80884 PRELIMINARY; PRT; 90 AA.  
AC Q80884;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16; TISSUE=Cervical tissue;  
RA Haegert D.G., Galutira D.F., Younghusband B.H.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U14513; AAB60567.2; -.  
DR GO:0042025; C:host cell nucleus; IEA.  
DR GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 90 AA; 11021 MW; 47F42BBEFAACCC01 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 7e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
DB 14 RDGNPYAVCDKCLKFYISKISEY 35

## RESULT 4

Q80885 ID Q80885 PRELIMINARY; PRT; 90 AA.  
AC Q80885;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16; TISSUE=Cervical tissue;  
RA Haegert D.G., Galutira D.F., Younghusband B.H.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U14514; AAB60568.2; -.  
DR GO:0042025; C:host cell nucleus; IEA.  
DR GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.

FT NON\_TER 1 1  
FT NON\_TER 90 90  
SQ SEQUENCE 90 AA; 10964 MW; BC2531643ACBA76C CRC64;

Query Match 100.0%; Score 125; DB 2; Length 90;  
Best Local Similarity 100.0%; Pred. No. 7e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
DB 14 RDGNPYAVCDKCLKFYISKISEY 35

## RESULT 5

Q80887 ID Q80887 PRELIMINARY; PRT; 91 AA.  
AC Q80887;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10566;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=HPV16; TISSUE=Cervical tissue;  
RA Haegert D.G., Galutira D.F., Younghusband B.H.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U14515; AAB60570.1; -.  
DR GO:0042025; C:host cell nucleus; IEA.  
DR GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON\_TER 1 1  
FT NON\_TER 91 91  
SQ SEQUENCE 91 AA; 11136 MW; 22PDF3EA185ACBA7 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 7e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
DB 14 RDGNPYAVCDKCLKFYISKISEY 35

## RESULT 6

Q919B2 ID Q919B2 PRELIMINARY; PRT; 99 AA.  
AC Q919B2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16 cervical cancer isolates from Australia and New Caledonia.";  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL; AF404704; AAL01365.1; -.  
DR GO:0042025; C:host cell nucleus; IEA.  
DR GO:0003677; F:DNA binding; IEA.  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
FT NON\_TER 1 1

FT NON\_TER 99 99  
SQ SEQUENCE 99 AA; 12005 MW; C2B96025EC370E38 CRC64;  
Query Match 100.0%; Score 125; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 7.7e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RDGNPYAVCDKCLFKFYISKISEY 22  
|||||  
Db 31 RDGNPYAVCDKCLFKFYISKISEY 52  
RESULT 7  
QY19D6 PRELIMINARY; PRT; 103 AA.  
AC QY19D6; (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
CX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL; AF404692; AAL01342.1; -  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
DR NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 103 AA; 12422 MW; 6F90CBA1F25449B CRC64;  
Query Match 100.0%; Score 125; DB 2; Length 103;  
Best Local Similarity 100.0%; Pred. No. 8e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RDGNPYAVCDKCLFKFYISKISEY 22  
|||||  
Db 7 RDGNPYAVCDKCLFKFYISKISEY 28

RESULT 8  
QY19B4 PRELIMINARY; PRT; 130 AA.  
AC QY19B4;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
CX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL; AF404703; AAL01363.1; -  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
DR NON\_TER 1  
FT NON\_TER 1

SQ SEQUENCE 130 AA; 15792 MW; B6C2147D227EEDDC CRC64;  
Query Match 100.0%; Score 125; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RDGNPYAVCDKCLFKFYISKISEY 22  
|||||  
Db 34 RDGNPYAVCDKCLFKFYISKISEY 55  
RESULT 9  
QY19B8 PRELIMINARY; PRT; 130 AA.  
AC QY19B8;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
CX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL; AF404701; AAL01359.1; -  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
DR NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 130 AA; 15775 MW; 92D3C07BF96B092F CRC64;  
Query Match 100.0%; Score 125; DB 2; Length 130;  
Best Local Similarity 100.0%; Pred. No. 1e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RDGNPYAVCDKCLFKFYISKISEY 22  
|||||  
Db 34 RDGNPYAVCDKCLFKFYISKISEY 55

RESULT 10  
QY19C0 PRELIMINARY; PRT; 130 AA.  
AC QY19C0;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE E6 protein (Fragment).  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
CX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21846229; PubMed=11857370;  
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
RT "Sequence variation and physical state of human papillomavirus type 16  
RT cervical cancer isolates from Australia and New Caledonia.";  
RL Int. J. Cancer 97:868-874(2002).  
DR EMBL; AF404700; AAL01357.1; -  
DR GO; GO:0042025; C:host cell nucleus; IEA.  
DR GO; GO:0003677; F:DNA binding; IEA.  
DR InterPro; IPR001334; E6.  
DR Pfam; PF00518; E6; 1.  
DR NON\_TER 1  
FT NON\_TER 1  
SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYISKISEY 22  
 |||||  
 Db 34 RDGNPYAVCDKCLKFYISKISEY 55

## RESULT 11

Q919C2 ID Q919C2 PRELIMINARY; PRT; 130 AA.  
 AC Q919C2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE E6 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21846229; PubMed=11857370;  
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
 RT "Sequence variation and physical state of human papillomavirus type 16  
 RT cervical cancer isolates from Australia and New Caledonia.";  
 RL Int. J. Cancer 97:868-874(2002).  
 DR EMBL; AF404699; AAL01355.1; --  
 DR GO; GO:0042025; C:host cell nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR001334; E6.  
 DR Pfam; PF00518; E6; 1.  
 FT NON TER 1  
 SQ SEQUENCE 130 AA; 15779 MW; 26D0147D396B0929 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYISKISEY 22  
 |||||  
 Db 34 RDGNPYAVCDKCLKFYISKISEY 55

## RESULT 12

Q919C8 ID Q919C8 PRELIMINARY; PRT; 130 AA.  
 AC Q919C8;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE E6 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21846229; PubMed=11857370;  
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
 RT "Sequence variation and physical state of human papillomavirus type 16  
 RT cervical cancer isolates from Australia and New Caledonia.";  
 RL Int. J. Cancer 97:868-874(2002).  
 DR EMBL; AF404699; AAL01355.1; --  
 DR GO; GO:0042025; C:host cell nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR001334; E6.  
 DR Pfam; PF00518; E6; 1.  
 FT NON TER 1  
 SQ SEQUENCE 130 AA; 15778 MW; 2830147D378B0DC9 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYISKISEY 22  
 |||||  
 Db 34 RDGNPYAVCDKCLKFYISKISEY 55

## RESULT 13

Q919D0 ID Q919D0 PRELIMINARY; PRT; 130 AA.  
 AC Q919D0;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE E6 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21846229; PubMed=11857370;  
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
 RT "Sequence variation and physical state of human papillomavirus type 16  
 RT cervical cancer isolates from Australia and New Caledonia.";  
 RL Int. J. Cancer 97:868-874(2002).  
 DR EMBL; AF404699; AAL01355.1; --  
 DR GO; GO:0042025; C:host cell nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR001334; E6.  
 DR Pfam; PF00518; E6; 1.  
 FT NON TER 1  
 SQ SEQUENCE 130 AA; 15735 MW; 9EFB30EEDCA21AF3 CRC64;

Query Match 100.0%; Score 125; DB 2; Length 130;  
 Best Local Similarity 100.0%; Pred. No. 1e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYISKISEY 22  
 |||||  
 Db 34 RDGNPYAVCDKCLKFYISKISEY 55

## RESULT 14

Q919D2 ID Q919D2 PRELIMINARY; PRT; 138 AA.  
 AC Q919D2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE E6 protein (Fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21846229; PubMed=11857370;  
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
 RT "Sequence variation and physical state of human papillomavirus type 16  
 RT cervical cancer isolates from Australia and New Caledonia.";  
 RL Int. J. Cancer 97:868-874(2002).  
 DR EMBL; AF404699; AAL01355.1; --  
 DR GO; GO:0042025; C:host cell nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR001334; E6.  
 DR Pfam; PF00518; E6; 1.  
 FT NON TER 1  
 SQ SEQUENCE 138 AA; 16696 MW; 481E5AEA90895FC2 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.1e-10; Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
 Db 42 RDGNPYAVCDKCLKFYISKISEY 63

RESULT 15

Q919B6 Q919B6 PRELIMINARY; PRT; 143 AA.  
 AC Q919B6;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE E6 protein (fragment).  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21846229; PubMed=11857370;  
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
 RT "Sequence variation and physical state of human papillomavirus type 16  
 cervical cancer isolates from Australia and New Caledonia."  
 RL Int. J. Cancer 97:868-874(2002).  
 DR EMBL; AF404702; AAL01361.1;  
 DR GO; GO:0042025; C:host cell nucleus; IEA.  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR001334; E6.  
 DR Pfam; PF00518; E6; 1.  
 FT NON TER 1  
 SQ SEQUENCE 143 AA; 17272 MW; 071F14EE3E6BE2AC CRC64;

Query Match 100.0%; Score 125; DB 2; Length 143;  
 Best Local Similarity 100.0%; Pred. NC. 1.1e-10;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
 Db 47 RDGNPYAVCDKCLKFYISKISEY 68

Search completed: November 22, 2004, 20:31:48  
 Job time : 128.5 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:19:30 ; Search time 23.5 Seconds  
(without alignments)  
90.075 Million cell updates/sec

Title: US-10-612-818-4

Perfect score: 125  
Sequence: 1 RDGNPYAVCDKCLKFYISKISEY 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79.\*

1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	158	1	protein E6 - human
2	102	81.6	149	1	E6 protein - human
3	96	76.8	151	1	E6 protein - human
4	90	72.0	149	1	E6 protein - human
5	89	71.2	148	2	E6 protein - human
6	89	71.2	148	2	E6 protein - human
7	88	70.4	149	1	E6 protein - human
8	87	69.6	149	1	E6 protein - human
9	84	67.2	150	2	E6 protein - human
10	82	65.6	191	1	E6 protein - human
11	79	63.2	158	1	E6 protein - human
12	77	61.6	155	1	E6 protein - human
13	77	61.6	155	1	E6 protein - human
14	76	60.8	158	1	E6 protein - human
15	74	59.2	154	2	E6 protein - human
16	72	57.6	148	2	E6 protein - human
17	72	57.6	153	2	E6 protein - human
18	72	57.6	154	2	E6 protein - human
19	72	57.6	155	2	E6 protein - human
20	71	56.8	150	1	E6 protein - human
21	71	56.8	158	1	E6 protein - human
22	65	52.0	142	2	E6 protein - human
23	65	52.0	158	2	E6 protein - human
24	62	49.6	154	2	E6 protein - human
25	59	47.2	153	1	E6 protein - human
26	58	46.4	150	1	E6 protein - human
27	54.5	43.6	1378	2	zinc finger protei
28	54.5	43.6	1571	2	zinc finger protei
29	53	42.4	150	1	E6 protein - human

30 51 40.8 159 1 S15614  
31 51 40.8 159 2 S36497  
32 51 40.8 407 2 B39240  
33 51 40.8 446 2 F90332  
34 51 40.8 1108 2 D96798  
35 50.5 40.4 150 1 W6WL31  
36 49 39.2 159 2 A85022  
37 47 37.6 392 2 A05025  
38 47 37.6 420 2 A72298  
39 47 37.6 431 2 T37621  
40 46.5 37.2 110 2 S38067  
41 46.5 37.2 110 2 S50345  
42 46.5 37.2 150 1 W6WL44  
43 46 36.8 172 2 B82047  
44 46 36.8 150 1 W6WL13  
45 46 36.8 518 2 B86372

#### ALIGNMENTS

##### RESULT 1

W6WLHS  
protein E6 - human papillomavirus type 16  
C:Species: human papillomavirus type 16  
C:Date: 28-May-1995 #sequence\_revision 28-May-1996 #text\_change 09-Jul-2004  
C:Accession: A03682; F10427  
R:Seedorf, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.  
Virology 145, 181-185, 1995  
A:Title: Human papillomavirus type 16 DNA sequence.  
A:Reference number: A22355; MUID:85246220; PMID:2990099  
A:Accession: A03682  
A:Molecule type: DNA  
A:Residues: 1-158 <SER>  
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032  
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.  
J. Virol. 65, 2093-2097, 1991  
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level  
A:Reference number: Z17014; MUID:91162763; PMID:1848319  
A:Accession: T10427  
A:Status: Preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-158 <KEN>  
A:Cross-references: EMBL:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032  
C:Genetics:  
A:Gene: E6  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:37-73/Region: zinc finger CCCC motif  
F:110-146/Region: zinc finger CCCC motif

Query Match 100.0%; Score 125; DB 1; Length 158;  
Best Local Similarity 100.0%; Pred. No. 1.8e-10;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
|||||  
DB 62 RDGNPYAVCDKCLKFYISKISEY 83

##### RESULT 2

W6WL35  
E6 protein - human papillomavirus type 35  
C:Species: human papillomavirus type 35  
A:Note: host Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C:Accession: E40824; S36521  
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.  
Virology 186, 770-776, 1992  
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillom  
A:Reference number: A40824; MUID:92124753; PMID:1310198  
A:Accession: E40824  
A:Status: translation not shown

A:Molecule type: DNA  
A:Residues: 1-149 <MAR>  
A:Cross-references: UNIPROT:P27228; GB:M74117; NID:G333050; PIDN:AAA46966.1; PID:G333051  
R:Delius, H.; Hofmann, B.  
Submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36521  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-149 <DEL>  
A:Cross-references: EMBL:X74477; NID:G396997; PIDN:CAA52561.1; PID:G396998  
A:Experimental source: strain 35H  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:30-66/Region: zinc finger CCCC motif  
F:103-139/Region: zinc finger CCCC motif

Query Match 81.6%; Score 102; DB 1; Length 149;  
Best Local Similarity 81.8%; Pred. No. 3e-07;  
Matches 18; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
|||:|||||:|||||  
Db 55 REQQPYGVCMKCLKFYISKISEY 76

RESULT 3  
W6WL51  
E6 protein - human papillomavirus type 51  
C:Species: human papillomavirus type 51  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: E40415  
R:Jung, O.; Crum, C.P.; Silverstein, S.J.  
J. Virol. 65, 4216-4225, 1991  
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type 51  
A:Reference number: A40415; MUID:91303675; PMID:1649326  
A:Accession: E40415  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-151 <LUN>  
A:Cross-references: UNIPROT:P26554; GB:M62877  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:30-66/Region: zinc finger CCCC motif  
F:103-139/Region: zinc finger CCCC motif

Query Match 76.8%; Score 96; DB 1; Length 151;  
Best Local Similarity 77.3%; Pred. No. 2.2e-06;  
Matches 17; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
|||:|||||:|||||  
Db 55 RDNNPYAVCKQLLFYISKIREY 76

RESULT 4  
W6WL58  
E6 protein - human papillomavirus type 58  
C:Species: human papillomavirus type 58  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C:Accession: E36779  
R:Kirii, Y.; Iwamoto, S.; Matsukura, T.  
Virology 185, 424-427, 1991  
A:Title: Human papillomavirus type 58 DNA sequence.  
A:Reference number: A36779; MUID:92024102; PMID:1656594  
A:Accession: E36779  
A>Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-149 <KIR>  
A:Cross-references: UNIPROT:P26555; GB:D90400; NID:G222386; PIDN:BAA31845.1; PID:G333709

C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding, early protein; zinc finger  
F:30-66/Region: zinc finger CCCC motif  
F:103-139/Region: zinc finger CCCC motif

Query Match 72.0%; Score 90; DB 1; Length 149;  
Best Local Similarity 72.7%; Pred. No. 1.5e-05;  
Matches 16; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
|||:|||||:|||||  
Db 55 RDGNPFYAVCKVCLRLLSKISEY 76

## RESULT 5

A61237

E6 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C:Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 03-May-1996

C:Accession: A61237

R:Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U.  
Int. J. Cancer 48, S16-S22, 1991

A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma  
A:Reference number: A61237; MUID:91258022; PMID:1646174

A:Accession: A61237

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <TAK>

C:Superfamily: papillomavirus E6 protein

Query Match 71.2%; Score 89; DB 2; Length 148;  
Best Local Similarity 72.7%; Pred. No. 2.1e-05;  
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
|||:|||||:|||||  
Db 55 RDNNPYGVCMCLRFSLSKISEY 76

## RESULT 6

S36573

E6 protein - human papillomavirus type 52

C:Species: human papillomavirus type 52

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S36573

R:Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36573

A:Molecule type: DNA

A:Residues: 1-148 <DEL>

A:Cross-references: UNIPROT:P36814; EMBL:X74481; NID:G397038; PIDN:CAA52585.1; PID:G39703

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 71.2%; Score 89; DB 2; Length 148;  
Best Local Similarity 72.7%; Pred. No. 2.1e-05;  
Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
|||:|||||:|||||  
Db 55 RDNNPYGVCMCLRFSLSKISEY 76

## RESULT 7

W6WL31

E6 protein - human papillomavirus type 31

C:Species: human papillomavirus type 31

A:Note: host Homo sapiens (man)

C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004

C:Accession: A32444

R:Goldsborough, M.D.; DiSilvestre, D.; Temple, G.F.; Lorincz, A.T.



```

Db      55  RDRSPYAACKRCRVIFYSKITEY  76
      ||:||||| |:|: |||||:|
RESULT 10
W6WLR1
E6 protein - rhesus papillomavirus (type 1)
C:Species: rhesus papillomavirus
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38503
R:Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A:Title: Characterization of the complete RHPV 1 genomic sequence and an integration loc
A:Reference number: A38503; UID:91135018; PMID:1847267
A:Accession: A38503
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-191 <OST>
A:Cross-references: UNIPROT:P22159; EMBL:M37717
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:60-96/Region: zinc finger CCCC motif
F:133-169/Region: zinc finger CCCC motif
      Query Match      65.6%; Score 82; DB 1; Length 191;
      Best Local Similarity 63.6%; Pred. No. 0.00025;
      Matches 14; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy      1  RDGNPYAVCDCLKFYKISEY  22
      ||||| |||||:|
Db      85  RQCKPYGVCPICLRIFYKIRKY  106
      ||||| |||||:|
RESULT 11
W6WL39
E6 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38502
R:Volpers, C.; Strecek, R.E.
Virology 181, 419-423, 1991
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A:Reference number: A38502; UID:91135017; PMID:1847266
A:Accession: A38502
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <VOL>
A:Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif
      Query Match      63.2%; Score 79; DB 1; Length 158;
      Best Local Similarity 61.9%; Pred. No. 0.00057;
      Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy      1  RDGNPYAVCDCLKFYKISE  21
      ||||| |||||:|
Db      57  RDGEPLAACQSCIKFYAKIRE  77
      ||||| |||||:|
RESULT 12
W6WL43
E6 protein - human papillomavirus type 43
C:Species: human papillomavirus type 43
A:Note: host Homo sapiens (man)
C:Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C:Accession: A34144
R:Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
A:Title: Cloning and partial DNA sequencing of two new human papillomavirus types associ

```

A:Reference number: A34144; MUID:89259065; PMID:2542593

A:Accession: A34144

A:Molecule type: DNA

A:Residues: 1-155 <LOE>

A:Cross-references: UNIPROT:PI9709; GB:M27022; NID:g341596; PIDN:AAA63453.1; PID:g703247

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:31-67/Region: zinc finger CCCC motif

F:104-140/Region: zinc finger CCCC motif

Query Match 61.6%; Score 77; DB 1; Length 155;

Best Local Similarity 59.1%; Pred. No. 0.0011;

Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22

DB 56 RDGYPFAACLAQLQFHGKISQY 77

#### RESULT 13

W6WLP56

E6 protein - human papillomavirus type 56

C:Species: human papillomavirus type 56

C>Date: 31-Dec-1991 #sequence\_revision 31-Dec-1991 #text\_change 09-Jul-2004

C:Accession: A33377; S36579

R:Loerincz, A. T.; Quinn, A. P.; Goldsborough, M. D.; McAllister, P.; Temple, G. F.

J. Gen. Virol. 70, 3099-3104, 1989

A:Title: Human papillomavirus type 56: a new virus detected in cervical cancers.

A:Reference number: A33377; MUID:90063558; PMID:2555440

A:Accession: A33377

A:Molecule type: DNA

A:Residues: 1-155 <LOE>

A:Cross-references: UNIPROT:P24836

R:DeLiuss, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36579

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-155 <DEL>

A:Cross-references: EMBL:X74483; NID:g397053; PIDN:CAA52596.1; PID:g397054

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; transforming protein; zinc finger

F:33-69/Region: zinc finger CCCC motif

F:106-142/Region: zinc finger CCCC motif

Query Match 61.6%; Score 77; DB 1; Length 155;

Best Local Similarity 63.6%; Pred. No. 0.0011;

Matches 14; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22

DB 58 RDDFPYAVCRVCLLFYSKRY 79

#### RESULT 14

W6WLP56

E6 protein - human papillomavirus type ME180 (provirus)

C:Species: human papillomavirus type ME180

A:Note: host Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C:Accession: C40509

R:Reuter, S.; DeLiuss, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.

J. Virol. 65, 5564-5568, 1991

A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma

A:Reference number: A40509; MUID:91374616; PMID:1716694.

A:Accession: C40509

A>Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-158 <REU>

A:Cross-references: UNIPROT:P27962; GB:M73258

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; zinc finger

F:32-68/Region: zinc finger CCCC motif

F:105-141/Region: zinc finger CCCC motif

Query Match 60.8%; Score 76; DB 1; Length 158;

Best Local Similarity 61.9%; Pred. No. 0.0015;

Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 21

DB 57 RDGVPAAACQSCIKFYAKIRE 77

#### RESULT 15

S36527

E6 protein - human papillomavirus type 53

C:Species: human papillomavirus type 53

C>Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C:Accession: S36527

R:DeLiuss, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36527

A:Molecule type: DNA

A:Residues: 1-154 <DEL>

A:Cross-references: UNIPROT:P36815; EMBL:X74482; NID:g397046; PIDN:CAA52591.1; PID:g397047

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match 59.2%; Score 74; DB 2; Length 154;

Best Local Similarity 68.4%; Pred. No. 0.0028;

Matches 13; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYSKI 19

DB 59 RDGYPYGVCKFCLLFYSKV 77

Search completed: November 22, 2004, 20:32:42

Job time : 24.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:32:01 ; Search time 97.5 Seconds  
(without alignments)  
79.906 Million cell updates/sec

Title: US-10-612-818-4

Perfect score: 125

Sequence: 1 RDGNPYAVCDKCLKFYKISEY 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
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5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
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13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	22	16	US-10-612-818-4
2	125	100.0	151	14	Sequence 4, Appli
3	125	100.0	171	16	Sequence 6, Appli
4	125	100.0	266	9	Sequence 2, Appli
5	125	100.0	273	13	Sequence 1, Appli
6	125	100.0	292	13	Sequence 4, Appli
7	125	100.0	371	13	Sequence 10, Appl
8	125	100.0	390	13	Sequence 6, Appli
9	109	87.2	20	16	Sequence 14, Appl
10	71	56.8	172	16	Sequence 11, Appl
11	71	56.8	278	13	Sequence 6, Appli
12	71	56.8	383	13	Sequence 21, Appl
13	61	48.8	10	8	Sequence 23, Appl
					Sequence 237, App

14	57	45.6	9	8	US-08-344-824-346	Sequence 346, App
15	56	44.8	462	15	US-10-424-599-252512	Sequence 252512, A
16	54.5	43.6	95	15	US-10-425-114-67951	Sequence 67951, A
17	52.5	42.0	209	16	US-10-767-701-61305	Sequence 61305, A
18	52.5	42.0	315	17	US-10-425-115-281736	Sequence 281736, A
19	52.5	42.0	1082	16	US-10-437-963-167162	Sequence 167162, A
20	51	40.8	1103	17	US-10-739-930-6660	Sequence 6660, Ap
21	50	40.0	154	15	US-10-425-114-54840	Sequence 54840, A
22	50	40.0	300	15	US-10-424-599-233668	Sequence 233668, A
23	50	40.0	326	15	US-10-425-114-44352	Sequence 44352, A
24	49.5	39.6	134	15	US-10-424-599-198743	Sequence 198743, A
25	49.5	39.6	144	14	US-10-829-386-28819	Sequence 28819, A
26	49.5	39.6	313	9	US-09-864-761-43142	Sequence 43142, A
27	49.5	39.6	388	9	US-09-842-777-12	Sequence 12, Appl
28	49.5	39.6	1086	16	US-10-437-963-104962	Sequence 104962, A
29	49.5	39.6	1158	16	US-10-437-963-126051	Sequence 126051, A
30	49.5	39.6	1464	9	US-09-842-777-10	Sequence 10, Appl
31	49.5	39.6	1523	14	US-10-205-219-135	Sequence 135, App
32	49.5	39.6	1523	15	US-10-173-999-123	Sequence 123, App
33	49.5	39.6	1569	15	US-10-334-143-67	Sequence 67, Appl
34	49.5	39.6	1685	15	US-10-376-774-2691	Sequence 2691, Ap
35	49	39.2	135	17	US-10-739-930-10865	Sequence 10865, A
36	49	39.2	136	16	US-10-767-701-51604	Sequence 51604, A
37	49	39.2	136	17	US-10-425-115-353730	Sequence 353730, A
38	49	39.2	137	16	US-10-437-963-143525	Sequence 143525, A
39	49	39.2	167	15	US-10-425-114-64865	Sequence 64865, A
40	49	39.2	174	17	US-10-425-115-351731	Sequence 351731, A
41	49	39.2	451	15	US-10-424-599-246501	Sequence 246501, A
42	49	39.2	458	15	US-10-425-114-38721	Sequence 38721, A
43	49	39.2	463	15	US-10-282-122A-74636	Sequence 74636, A
44	49	39.2	467	16	US-10-437-963-163687	Sequence 163687, A
45	48.5	39.8	427	17	US-10-425-115-304190	Sequence 304190, A

## ALIGNMENTS

RESULT 1  
US-10-612-818-4  
Sequence 4, Application US/10612818  
Publication No. US20040110925A1  
GENERAL INFORMATION:  
APPLICANT: Impact Diagnostics  
APPLICANT: Impact Diagnostics  
TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruses  
TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil  
TITLE OF INVENTION: Associated Cancers  
FILE REFERENCE: 3352-2-2  
CURRENT APPLICATION NUMBER: US/10/612,818  
CURRENT FILING DATE: 2003-07-01  
PRIOR APPLICATION NUMBER: US 60/394,172  
PRIOR FILING DATE: 2002-07-02  
PRIOR APPLICATION NUMBER: US 09/828,645  
PRIOR FILING DATE: 2001-04-05  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 4  
LENGTH: 22  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Derived from the E6 early coding region of HPV 16  
US-10-612-818-4  
Query Match 100.0%; Score 125; DB 16; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.6e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RDGNPYAVCDKCLKFYKISEY 22  
DB 1 RDGNPYAVCDKCLKFYKISEY 22

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RESULT 2
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerp Innovatiecentrum
; TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match 100.0%; Score 125; DB 14; Length 151;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 55 RDGNPYAVCDKCLKFYISKISEY 76

RESULT 3
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match 100.0%; Score 125; DB 16; Length 171;
Best Local Similarity 100.0%; Pred. No. 1.3e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 67 RDGNPYAVCDKCLKFYISKISEY 88

RESULT 4
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A

; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match 100.0%; Score 125; DB 9; Length 266;
Best Local Similarity 100.0%; Pred. No. 2e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 5
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match 100.0%; Score 125; DB 13; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
DB 168 RDGNPYAVCDKCLKFYISKISEY 189

RESULT 6
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
```

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; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence: peptide E6 61-80
US-10-476-570-11

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; LENGTH: 172
; TYPE: PRT
; ORG: 00000000
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-6

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Query Match 56.8%; Score 71; DB 16; Length 172;  
Best Local Similarity 57.1%; Pred. No. 0.015;  
Matches 12; Conservative 3; Mismatches 6; Indels

QY 1 RDGNPYAVCDKCLKFYKISE 21  
63 RDSIPHAACHKCIDFYRIRE 83  
DB

```

RESULT 11
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Gabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-21

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Query Match 56.8%; Score 71; DB 13; Length 278;  
Best Local Similarity 57.1%; Pred. No. 0.024;  
Matches 12: Conservative 3; Mismatches 6; Indels

QY 1 RDGNPYAVCDKCLKFYKISE 21  
|||:|:|:|:|:|:|:  
Db 168 RDSIPHAACHKCIDFYSRIRE 188

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RESULT 12
US/10-000-903-23
/ Sequence 23, Application US/10000903
/ Publication No. US20020182221A1
/ GENERAL INFORMATION:
/ APPLICANT: Bruck, Claudine
/ APPLICANT: Cabezon Silva, Teresa
/ APPLICANT: Delisse, Anne-Marie Eva Fernando
/ APPLICANT: Gerard, Catherine Marie Ghislaine
/ APPLICANT: Lombardo-Bencheikh, Angela
/ TITLE OF INVENTION: Vaccine
/ FILE REFERENCE: B45107
/ CURRENT APPLICATION NUMBER: US/10/000,903
/ CURRENT FILING DATE: 2001-10-01
/ PRIOR APPLICATION NUMBER: PCT/EP98/05285
/ PRIOR FILING DATE: 1998-08-17
/ PRIOR APPLICATION NUMBER: GB 9717953.5
/ PRIOR FILING DATE: 1997-08-22
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 23
/ LENGTH: 383

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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-23

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Query Match 56.8%; Score 71; DB 13; Length 383;  
Best Local Similarity 57.1%; Pred. No. 0.033;  
Matches 12; Conservative 3; Mismatches 6; Indels 0; Caps 0;

QY 1 RDGNPYAVCDKCLKFYSKISE 21  
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Dd 168 RDSIPHAACHKCIDFYSRIRE 188

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1  RESULT 13
2  US-08-344-824-237
3  ; Sequence 237, Application US/08344824
4  ; Publication No. US20030152580A1
5  ; GENERAL INFORMATION:
6  ; APPLICANT: SETTE, Alessandro
7  ; APPLICANT: SIDNEY, John
8  ; TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES
9  ; NUMBER OF SEQUENCES: 399
10 ; CORRESPONDENCE ADDRESS:
11 ; ADDRESSEE: Townsend and Townsend Kourie and Crew
12 ; STREET: One Market Plaza, Steuart Street Tower, 20th
13 ; STREET: Floor
14 ; CITY: San Francisco
15 ; STATE: California
16 ; COUNTRY: USA
17 ; ZIP: 94105
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/08/344,824
25 ; FILING DATE: 23-NOV-1994
26 ; CLASSIFICATION: 514
27 ; PRIOR APPLICATION DATA:
28 ; APPLICATION NUMBER: US 08/278,634
29 ; FILING DATE: 21-JUL-1994
30 ; ATTORNEY/AGENT INFORMATION:
31 ; NAME: Bastian, Kevin L.
32 ; REGISTRATION NUMBER: 34,774
33 ; REFERENCE/DOCKET NUMBER: 14137-80-1
34 ; TELECOMMUNICATION INFORMATION:
35 ; TELEPHONE: (415) 543-9600
36 ; TELEFAX: (415) 543-5043
37 ; INFORMATION FOR SEQ ID NO: 237:
38 ; SEQUENCE CHARACTERISTICS:
39 ; LENGTH: 10 amino acids
40 ; TYPE: amino acid
41 ; STRANDEDNESS: single
42 ; TOPOLOGY: linear
43 ; MOLECULE TYPE: DNA (genomic)
44 ; PS-08-144-824-237

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Query Match      48.8%; Score 61; DB 8; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 4 NPYAVCDKCL 13  
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Db 1 NPYAVCDKCL 10

RESULT 14  
US-08-344-824-346  
; Sequence 346. Application US/08344824  
; Publication No. US20030152580A1  
; GENERAL INFORMATION:  
; APPLICANT: SETTE, Alessandro

APPLICANT: SIDNEY, John  
TITLE OF INVENTION: HLA BINDING PEPTIDES AND THEIR USES  
NUMBER OF SEQUENCES: 399  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Kourie and Crew  
STREET: One Market Plaza, Steuart Street tower, 20th  
STREET: Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/344,824  
FILING DATE: 23-NOV-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/278,634  
FILING DATE: 21-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 14137-80-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 346:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-344-824-346

Query Match 45.6%; Score 57; DB 8; Length 9;  
Best Local Similarity 100.0%; Pred.No. 1.4e+06;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NPYAVCDKC 12  
Db 1 NPYAVCDKC 9

RESULT 15  
US-10-424-599-252512  
Sequence 252512, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: Kovalic David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 252512  
LENGTH: 462  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (1)..(462)  
OTHER INFORMATION: unsure at all Xaa locations  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_70045C.1.pep

US-10-424-599-252512  
Query Match 44.8%; Score 56; DB 15; Length 462;  
Best Local Similarity 47.4%; Pred.No. 6.9;  
Matches 9; Conservative 3; Mismatches 7; Indels 0; Gaps 0;  
QY 3 GNPYAVCDKCLKFYISKISE 21  
Db 227 GKPVRVCDSCFVKLNKVAE 245  
Search completed: November 22, 2004, 20:48:54  
Job time : 99.5 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:20:21 ; Search time 27.5 Seconds  
(without alignments)  
53.054 Million cell updates/sec

Title: US-10-612-818-4

Perfect score: 125

Sequence: 1 RDGNPYAVCDKCLKFYISKISEY 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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  - 2: /cgn2\_6/prodata/1/iaa/5B COMB.pep.\*
  - 3: /cgn2\_6/prodata/1/iaa/6A COMB.pep.\*
  - 4: /cgn2\_6/prodata/1/iaa/6B COMB.pep.\*
  - 5: /cgn2\_6/prodata/1/iaa/PCTUS COMB.pep.\*
  - 6: /cgn2\_6/prodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	125	100.0	158	4	US-09-980-523A-2
2	125	100.0	162	1	US-08-316-239B-3
3	125	100.0	162	1	US-08-316-239B-4
4	125	100.0	172	3	US-08-860-165-14
5	125	100.0	172	3	US-09-359-382-14
6	125	100.0	266	3	US-08-860-165-10
7	125	100.0	266	4	US-09-359-382-10
8	125	100.0	266	4	US-09-357-309A-1
9	125	100.0	273	3	US-09-485-885-4
10	125	100.0	292	3	US-09-485-885-10
11	125	100.0	371	3	US-09-485-885-6
12	125	100.0	390	3	US-09-485-885-14
13	114	91.2	172	3	US-08-860-165-12
14	114	91.2	172	3	US-09-359-382-12
15	103	82.4	20	2	US-08-934-915-162
16	71	56.8	158	2	US-08-247-904B-10
17	71	56.8	158	3	US-08-767-942A-19
18	71	56.8	271	1	US-08-117-083-14
19	71	56.8	278	3	US-09-485-885-21
20	71	56.8	368	3	US-09-000-094-20
21	71	56.8	368	4	US-10-011-749-20
22	71	56.8	368	4	US-09-000-004-20
23	71	56.8	375	3	US-09-000-094-22
24	71	56.8	375	4	US-10-011-749-22
25	71	56.8	375	4	US-09-000-004-22
26	71	56.8	383	3	US-09-485-885-23
27	71	56.8	465	3	US-09-000-094-24

28	71	56.8	465	4	US-10-011-749-24	Sequence 24, Appl
29	71	56.8	465	4	US-09-000-004-24	Sequence 24, Appl
30	71	56.8	1587	3	US-09-000-094-46	Sequence 46, Appl
31	71	56.8	1587	4	US-10-011-749-46	Sequence 46, Appl
32	71	56.8	1587	4	US-09-000-004-46	Sequence 46, Appl
33	66	52.8	11	3	US-08-159-339A-1170	Sequence 1170, Ap
34	59	47.2	10	3	US-08-159-339A-561	Sequence 561, App
35	55	44.0	9	3	US-08-159-339A-74	Sequence 74, Appl
36	54	43.2	32	1	US-08-466-385-4	Sequence 4, Appl
37	54	43.2	32	3	US-08-164-768-4	Sequence 4, Appl
38	47	37.6	9	3	US-08-159-339A-229	Sequence 229, App
39	46	36.8	8	3	US-08-159-339A-1169	Sequence 1169, Ap
40	46	36.8	403	4	US-09-328-352-7791	Sequence 7791, Ap
41	45	36.0	9	3	US-08-159-339A-219	Sequence 219, App
42	45	36.0	524	4	US-03-408-020-10	Sequence 10, Appl
43	45	36.0	548	4	US-03-328-352-6605	Sequence 6605, Ap
44	44.5	35.6	135	4	US-09-513-999C-5846	Sequence 5846, Ap
45	44.5	35.6	3070	4	US-09-961-403-7	Sequence 7, Appl

## ALIGNMENTS

RESULT 1  
US-09-980-523A-2  
; Sequence 2, Application US/09980523A  
; Patent No. 6783763  
; GENERAL INFORMATION:  
; APPLICANT: CHOPPIN, JEANNINE  
; APPLICANT: BOURGAULT VILLADA, ISABELLE  
; APPLICANT: GUILLET, JEAN-GERARD  
; APPLICANT: CONNAN, FRANCINE  
; APPLICANT: FERRIES, ESTELLE  
; TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7  
; TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE  
; TITLE OF INVENTION: PARTICULARLY IN VACCINATION  
; FILE REFERENCE: WO81 AO INS  
; CURRENT APPLICATION NUMBER: US/09/980,523A  
; CURRENT FILING DATE: 2002-04-29  
; PRIOR APPLICATION NUMBER: PCT/FR00/01513  
; PRIOR FILING DATE: 2000-05-31  
; PRIOR APPLICATION NUMBER: FR 99/07012  
; PRIOR FILING DATE: 1999-06-03  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 158  
; TYPE: PRT  
; ORGANISM: Human Papillomavirus  
US-09-980-523A-2

Query Match 100.0%; Score 125; DB 4; Length 158;  
Best Local Similarity 100.0%; Pred. No. 1.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
DB 62 RDGNPYAVCDKCLKFYISKISEY 83

## RESULT 2

US-08-316-239B-3  
; Sequence 3, Application US/08316239B  
; Patent No. 5679509  
; GENERAL INFORMATION:  
; APPLICANT: Wheeler, Cosette M.  
; APPLICANT: Parmenter, Cheryl A.  
; TITLE OF INVENTION: Methods and a Diagnostic Aid for  
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an  
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and  
; TITLE OF INVENTION: Cervical Cancer  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-3

Query Match 100.0%; Score 125; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
Db 62 RDGNPYAVCDKCLKFYKISEY 83

RESULT 3
US-08-316-239B-4
; Sequence 4, Application US/08316239B
; Patent No. 5679509
; GENERAL INFORMATION:
; APPLICANT: Wheeler, Colette M.
; APPLICANT: Parmenter, Cheryl A.
; TITLE OF INVENTION: Methods and a Diagnostic Aid for
; Distinguishing a Subset of HPV that is Associated with an
; TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
; TITLE OF INVENTION: Cervical Cancer
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001

; ADDRESSEE: Jagtiani & Associates
; STREET: 6126 Rocky Way Court
; CITY: Centreville
; STATE: VA
; COUNTRY: USA
; ZIP: 20120-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,239B
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jagtiani, Ajay A.
; REGISTRATION NUMBER: 35,205
; REFERENCE/DOCKET NUMBER: UNNE-0001

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 817-9453
; TELEFAX: (703) 803-9387
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 162 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-316-239B-4

Query Match 100.0%; Score 125; DB 1; Length 162;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
Db 62 RDGNPYAVCDKCLKFYKISEY 83

RESULT 4
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
; US-08-860-165-14

Query Match 100.0%; Score 125; DB 3; Length 172;
Best Local Similarity 100.0%; Pred. No. 1.6e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22
Db 131 RDGNPYAVCDKCLKFYKISEY 152

RESULT 5
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
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EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU P0157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 14  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-359-382-14

Query Match 100.0%; Score 125; DB 3; Length 172;

Best Local Similarity 100.0%; Pred. No. 1.6e-11; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22

Db 131 RDGNPYAVCDKCLKFYISKISEY 152

#### RESULT 6

US-08-860-165-10

Sequence 10, Application US/08860165A

Patent No. 6004557

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: COX, John Cooper

APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRATER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA-VIRUS-ANTIGENS

FILE REFERENCE: 17227/130

CURRENT APPLICATION NUMBER: US/08/860,165A

CURRENT FILING DATE: 1997-09-22

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER FILING DATE: 1995-12-20

EARLIER APPLICATION NUMBER: AU P0157

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patent In Ver. 2.0

SEQ ID NO 10

LENGTH: 266

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion

US-08-860-165-10

Query Match 100.0%; Score 125; DB 3; Length 266;

Best Local Similarity 100.0%; Pred. No. 2.6e-11; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22

Db 62 RDGNPYAVCDKCLKFYISKISEY 83

#### RESULT 7

US-09-359-382-10

Sequence 10, Application US/09359382

Patent No. 6306397

GENERAL INFORMATION:

APPLICANT: EDWARDS, Stirling John

APPLICANT: COX, John Cooper

APPLICANT: WEBB, Elizabeth Ann

APPLICANT: FRATER, Ian

TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS

FILE REFERENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: US 08/860,165

EARLIER FILING DATE: 1997-09-22

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU P0157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patent In Ver. 2.0  
SEQ ID NO 10  
LENGTH: 266  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
US-09-359-382-10

Query Match 100.0%; Score 125; DB 3; Length 266;

Best Local Similarity 100.0%; Pred. No. 2.6e-11; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22

Db 62 RDGNPYAVCDKCLKFYISKISEY 83

#### RESULT 8

US-09-367-309A-1

Sequence 1, Application US/09367309A

Patent No. 6428807

GENERAL INFORMATION:

APPLICANT: MACFARLAN, RODERICK I.

APPLICANT: MALLIAROS, JIM

TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES

FILE REFERENCE: 012227/0149

CURRENT APPLICATION NUMBER: US/09/367309A

CURRENT FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: PCT/AU98/00080

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: AU PO 5178

PRIOR FILING DATE: 1997-02-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 1

LENGTH: 266

TYPE: PRT

ORGANISM: Human papillomavirus type 16

US-09-367-309A-1

Query Match 100.0%; Score 125; DB 4; Length 266;

Best Local Similarity 100.0%; Pred. No. 2.6e-11; Indels 0; Gaps 0;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22

Db 62 RDGNPYAVCDKCLKFYISKISEY 83

#### RESULT 9

US-09-485-885-4

Sequence 4, Application US/09485885

Patent No. 6342224

GENERAL INFORMATION:

APPLICANT: Bruck, Claudine

APPLICANT: Cabezon Silva, Teresa

APPLICANT: Delisse, Anne-Marie Eva Fernande

APPLICANT: Gerard, Catherine Marie Ghislaine

APPLICANT: Lombardo-Bencheikh, Angela

TITLE OF INVENTION: Vaccine

FILE REFERENCE: B45107

CURRENT APPLICATION NUMBER: US/09/485,885

CURRENT FILING DATE: 2000-02-18

PRIOR APPLICATION NUMBER: PCT/EP98/05285

PRIOR FILING DATE: 1998-08-17

PRIOR APPLICATION NUMBER: GB 9717953.5

PRIOR FILING DATE: 1997-08-22

NUMBER OF SEQ ID NOS: 23

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 4

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; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4
Query Match 100.0%; Score 125; DB 3; Length 273;
Best Local Similarity 100.0%; Pred. No. 2.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 168 RDGNPYAVCDKCLKFYISKISEY 189

RESULT 10
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
Query Match 100.0%; Score 125; DB 3; Length 292;
Best Local Similarity 100.0%; Pred. No. 2.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 187 RDGNPYAVCDKCLKFYISKISEY 208

RESULT 11
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6
Query Match 100.0%; Score 125; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 3.7e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 168 RDGNPYAVCDKCLKFYISKISEY 189

RESULT 12
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-14
Query Match 100.0%; Score 125; DB 3; Length 390;
Best Local Similarity 100.0%; Pred. No. 3.9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22
Db 187 RDGNPYAVCDKCLKFYISKISEY 208

RESULT 13
US-08-860-165-12
; Sequence 12, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-12
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Query Match 91.2%; Score 114; DB 3; Length 172;  
Best Local Similarity 100.0%; Pred. No. 7.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GNPVAVCDKCLKFYKISEY 22  
Db 2 GNPVAVCDKCLKFYKISEY 21

RESULT 14  
US-09-359-382-12  
; Sequence 12, Application US/09359382  
; Patent No. 6306397  
; GENERAL INFORMATION:  
; APPLICANT: EDWARDS, Stirling John  
; APPLICANT: COX, John Cooper  
; APPLICANT: WEBB, Elizabeth Ann  
; APPLICANT: FRAZER, Ian  
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
; FILE REFERENCE: 017227/0148  
; CURRENT APPLICATION NUMBER: US/09/359,382  
; CURRENT FILING DATE: 1999-07-23  
; EARLIER APPLICATION NUMBER: US 08/860,165  
; EARLIER FILING DATE: 1997-09-22  
; EARLIER APPLICATION NUMBER: PCT/AU95/00868  
; EARLIER FILING DATE: 1995-12-20  
; EARLIER APPLICATION NUMBER: AU P0157/94  
; EARLIER FILING DATE: 1994-12-20  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-09-359-382-12

Query Match 91.2%; Score 114; DB 3; Length 172;  
Best Local Similarity 100.0%; Pred. No. 7.8e-10;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GNPVAVCDKCLKFYKISEY 22  
Db 2 GNPVAVCDKCLKFYKISEY 21

RESULT 15  
US-08-934-915-162  
; Sequence 162, Application US/08934915  
; Patent No. 5932412  
; GENERAL INFORMATION:  
; APPLICANT: DILLNER, JOAKIM  
; APPLICANT: DILLNER, LENA  
; APPLICANT: CHENG, HWEI-MING  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN  
; TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,  
; TITLE OF INVENTION: 11, 15, 18, 31, 33 AND 56,  
; TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR  
; TITLE OF INVENTION: DIAGNOSTIC PURPOSES  
; NUMBER OF SEQUENCES: 193  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MASON & ASSOCIATES, P.A.  
; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500  
; CITY: CLEARWATER  
; STATE: FLORIDA  
; COUNTRY: U.S.A.  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Windows 3.0  
; SOFTWARE: Microsoft Word 6.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,915  
; FILING DATE: 22-SEP-1997

; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/949,836  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: LOUISE A. Foutch  
; REGISTRATION NUMBER: 37,133  
; REFERENCE/DOCKET NUMBER: 1946.6  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 813-538-3800  
; TELEFAX: 813-538-3820  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 162:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 20 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-934-915-162

Query Match 82.4%; Score 103; DB 2; Length 20;  
Best Local Similarity 90.0%; Pred. No. 3.8e-09;  
Matches 18; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RDGNPYAVCDKCLKFYKIS 20  
Db 1 RGNPNYAVCNKCLKFYKIS 20

Search completed: November 22, 2004, 20:33:42  
Job time : 28.5 secs

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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:14:12 ; Search time 113.5 Seconds  
(without alignments)  
69.533 Million cell updates/sec

Title: US-10-612-818-4  
Perfect score: 125  
Sequence: 1 RDGNFYAVCDKCLKFYKISEY 22

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23sep04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	125	100.0	22	8	ADI34603 HPV 16 E6
2	125	100.0	151	6	AAO22640 HPV-16 pr
3	125	100.0	151	6	AAO22636 HPV prote
4	125	100.0	151	8	ADO44072 Amino aci
5	125	100.0	158	2	AAR232766 HPV E6 pe
6	125	100.0	158	3	AAY92462 Human pap
7	125	100.0	158	4	AAB98420 Human pap
8	125	100.0	158	7	ADF09515 Human pap
9	125	100.0	158	8	ADL90078 Human pap
10	125	100.0	162	2	AAW35741 Human pap
11	125	100.0	162	2	AAW35742 Human pap
12	125	100.0	171	5	AAO22922 Human pap
13	125	100.0	172	2	AAR97563 Human pap
14	125	100.0	180	7	ADF1985 Human pap
15	125	100.0	188	2	AAR63865 HPV16 E6/
16	125	100.0	243	3	AAW99369 Papilloma
17	125	100.0	248	8	ADO44060 Amino aci
18	125	100.0	248	8	ADO44066 Amino aci
19	125	100.0	263	2	AAR27725 HPV 16 E6
20	125	100.0	266	2	AAR97561 Human pap
21	125	100.0	273	2	AAY25376 HPV fusio
22	125	100.0	273	2	AAY02632 Prot.D1/3
23	125	100.0	292	2	AAY25379 HPV fusio
24	125	100.0	292	2	AAY02635 CLYTA-E6-
25	125	100.0	371	2	AAY25377 HPV fusio

26	125	100.0	371	2	AA02633	Prot.D1/3
27	125	100.0	390	2	AA025381	HPV fusio
28	125	100.0	390	2	AA02637	CLYTA-E6E
29	120	96.0	151	3	AA057808	HPV-16 E6
30	114	91.2	172	2	AAR97562	Human pap
31	113	90.4	248	8	ADO44062	Amino aci
32	113	90.4	248	8	ADO44064	Amino aci
33	113	90.4	248	8	ADO44068	Amino aci
34	113	90.4	248	8	ADO44070	Peptide d
35	109	87.2	20	6	ABP70252	HPV E6 re
36	102	81.6	149	2	AAR40919	HPV E6 re
37	102	81.6	149	8	ADO44077	Amino aci
38	96	76.8	16	2	AAW29586	Peptide G
39	96	76.8	17	2	AAW29585	Peptide G
40	96	76.8	19	2	AAW29583	Peptide G
41	96	76.8	21	2	AAW29572	Peptide G
42	96	76.8	32	4	AAAB31109	A polyepi
43	96	76.8	32	4	AAAB31017	Polyepitc
44	96	76.8	151	8	ADO44080	Amino aci
45	91	72.8	15	2	AAW29587	Peptide G

## ALIGNMENTS

RESULT 1  
ADI34603  
ID ADI34603 standard; peptide; 22 AA.  
XX AC ADI34603;  
XX DT 22-APR-2004 (first entry)  
XX DE HPV 16 E6 early coding region derived peptide.  
XX KW HPV; E2; E6; E7; cancer; cellular abnormality.  
XX OS Human papillomavirus.  
XX EN WC0004005469-A2.  
XX PD 15-JAN-2004.  
XX PF 02-JUL-2003; 2003WO-US020887.  
XX PR 02-JUL-2002; 2002US-0394172P.  
XX ER 01-JUL-2003; 2003US-00612818.  
XX (IMPA-) IMPACT DIAGNOSTICS INC.  
Hu YX, Rosenfeld MJ;  
WPI; 2004-142978/14.  
New peptides from the E2, E6 or E7 proteins of human papillomavirus (HPV) 16 or 18, useful for detecting and/or diagnosing HPV-associated cellular abnormalities or cervical dysplasia or carcinoma.  
Claim 4; SEQ ID NO 4; 31pp; English.

The invention relates to an isolated protein sequence or peptide from the E2, E6 or E7 early coding region of human papillomavirus (HPV) that is soluble in an aqueous medium, and characterized by a relative lack of tryptophan, methionine and cysteine residues, and a relative abundance of glycine and asparagine residues. The protein sequences can be used in a method for detecting or diagnosing cancer or cellular abnormalities. The method involves reacting a sample of body fluid or tissue likely to contain antibodies with one or more protein sequences or peptides cited above, forming an antibody-peptide complex comprising at least one of the protein sequences or peptides and the sample antibodies, and detecting the antibody-peptide complex. The protein sequences and method are useful for detecting and/or diagnosing HPV-associated epithelial cell abnormalities, precancerous conditions and cancers, such as cervical





XX DE Amino acid sequence of a wild type HPV16 E6 protein.  
 XX DE  
 XX E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer;  
 KW cervical cancer; immune response; lower gastrointestinal tract cancer;  
 KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
 XX  
 OS Human papillomavirus type 16.  
 OS Synthetic.  
 OS  
 PN WO2004030636-A2.  
 XX  
 XX 15-APR-2004.  
 XX  
 XX 02-OCT-2003; 2003WO-US031726.  
 XX  
 XX 03-OCT-2002; 2002US-0415929P.  
 XX  
 XX (AMHP ) WYETH HOLDINGS CORP.  
 XX  
 XX Smith L, Cassetti MC;  
 XX  
 XX WPI; 2004-316328/29.  
 XX  
 XX New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 XX  
 XX Claim 1; Page 76-77; 101pp; English.  
 XX  
 CC The present sequence represents a wild type E6 protein from human  
 CC papillomavirus type 16 (HPV16), which is used to produce fusion proteins  
 CC of the invention. The specification describes human papillomavirus E6 and  
 CC E7 polypeptides, where the E7 polypeptide has mutations at any one or  
 CC more of the amino acids corresponding to amino acids 24, 26 or 91 of the  
 CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has  
 CC mutations at any one or more of the amino acids corresponding to amino  
 CC acids 63 or 106 of the sequence given in ADO44072. The polypeptides of  
 CC the invention are useful for treating or preventing human papillomavirus  
 CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins  
 CC and nucleic acids encoding the fusion proteins are useful for generating  
 CC immune responses against HPV. They are also useful for treating lower  
 CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of  
 CC the reproductive system, including penile and vulvar cancer.  
 XX  
 XX Sequence 151 AA;  
 SQ  
 Query Match 100.0%; Score 125; DB 8; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RDGNPYAVCDKCLFYKISEY 22  
 Db 55 RDGNPYAVCDKCLFYKISEY 76  
 RESULT 5  
 AAR22766  
 ID AAR22766 standard; peptide; 158 AA.  
 AC AAR22766;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 21-SEP-1992 (first entry)  
 XX  
 XX HPV E6 peptide.  
 DE  
 XX Human; papillomavirus; immunogenic; cervical; warts; carcinoma; cancer.  
 KW  
 XX Synthetic.  
 OS  
 OS Homo sapiens.  
 XX  
 XX WO9205248-A.  
 FN

XX 02-APR-1992.  
 PD  
 XX 26-SEP-1991; 91WO-US007081.  
 PF  
 XX 26-SEP-1990; 90US-00588384.  
 PR  
 XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
 PA  
 XX Thomas EK, Chen L, Blake J, Hellstrom K, Hellstrom I, Hu SL;  
 PI  
 XX WPI; 1992-132119/16.  
 XX  
 XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 - and  
 PT recombinant cells encoding them, useful in treatment and prophylaxis of  
 PT cervical warts or cancer resulting from HPV infection.  
 XX  
 XX Disclosure; Fig 7; 81pp; English.  
 PS  
 XX The peptide is the sequence of the human papillomavirus HPV 16 E6  
 CC nucleoprotein. Peptides corresponding to regions (pref. epitopic regions)  
 CC of HPV 16 E6 were synthesised by standard Merrifield synthesis. Examples  
 CC of such peptides are E6 1-20, 8-20, 119-134 or 148-158. Compositions  
 CC contg. these peptides, antibodies against the peptides, or recombinant  
 CC cells contg. the gene encoding the immuno- genic peptides may be utilised  
 CC in methods for inhibiting and treating HPV infection and tumour  
 CC initiation and progression e.g. in the prevention or retardation of  
 CC cervical warts and cervical carcinoma resulting from HPV infection. See  
 CC also AAR22767. (Updated on 25-MAR-2003 to correct PA field.) (Updated on  
 CC 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 158 AA;  
 SQ  
 Query Match 100.0%; Score 125; DB 2; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RDGNPYAVCDKCLFYKISEY 22  
 Db 62 RDGNPYAVCDKCLFYKISEY 83  
 RESULT 6  
 AAY82462  
 ID AAY82462 standard; protein; 158 AA.  
 XX  
 XX AAY82462;  
 AC  
 XX 30-JUN-2000 (first entry)  
 DT  
 XX Human papillomavirus E6 protein containing two zinc finger motifs.  
 DE  
 XX Chelated zinc finger; therapeutic; treatment; prophylaxis; MPV;  
 KW mammalian papillomavirus; antiviral; cytostatic; cervical cancer; lesion;  
 KW wart.  
 XX  
 XX Human papillomavirus.  
 OS  
 XX Key Location/Qualifiers  
 FH  
 FT Misc-difference 37..73 /note="forms a zinc finger motif"  
 FT Misc-difference 110..146 /note="forms a zinc finger motif"  
 FT  
 XX WO200014063-A1.  
 PN  
 XX 16-MAR-2000.  
 PD  
 XX 03-SEP-1999; 99WO-AU0000724.  
 XX  
 XX 04-SEP-1998; 98AU-00005733.  
 PR  
 XX 15-JUL-1999; 99AU-00001645.  
 PR  
 XX

PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
 PA (HUGH/) HUGHES E J L.  
 XX Bernard H, Tan YJ, Beerheide W, Ting AE, Sim WM;  
 PI WPI; 2000-356917/22.  
 XX  
 XX Polyulfide and dithionodisulfide agents, useful for the treatment or  
 PT prophylaxis of diseases caused by mammalian papillomavirus, are  
 PT disruptors of a chelated metal cation domain in an MPV gene encoded  
 PT protein.  
 XX  
 XX Disclosure; Fig 1; 78pp; English.  
 XX  
 XX The present invention describes an agent used in the treatment or  
 CC prophylaxis of a disease caused or exacerbated by MPV (mammalian  
 CC papillomavirus) comprising a compound capable of reducing, inhibiting or  
 CC otherwise decreasing the activity of a protein encoded by an MPV gene by  
 CC facilitating disruption of a chelated metal cation domain present in the  
 CC protein. An agent of the present invention can be used to treat cervical  
 CC cancer or its HPV associated precursor lesions or other HPV associated  
 CC cancers and/or warts. The present sequence represents a human  
 CC papillomavirus E6 protein containing two zinc finger motifs, as given in  
 CC the exemplification of the present invention  
 XX

Query Match 100.0%; Score 125; DB 3; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGNPYAVCDKCLKFYISKISEY 22  
 DB 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 7  
 AAB98420  
 ID AAB98420 standard; protein; 158 AA.  
 XX  
 XX AAB98420;  
 XX  
 XX 22-AUG-2001 (first entry)  
 XX  
 XX Human papillomavirus protein HPV16 E6.  
 DE  
 XX Human papillomavirus.  
 KW Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;  
 KW epitope; T cell; identification; vaccine; infection; genital wart;  
 KW neoplastic growth; antiviral.  
 XX  
 XX Human papillomavirus.  
 OS  
 XX WO200141799-A1.  
 XX  
 XX 14-JUN-2001.  
 XX  
 XX 11-DEC-2000; 2000WO-US033549.  
 XX  
 XX 10-DEC-1999; 99US-0172705P.  
 XX  
 XX 15-AUG-2000; 2000US-00641528.  
 XX  
 XX (EPIM-) EPIMMUNE INC.  
 XX  
 XX Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;  
 PI WPI; 2001-381497/40.  
 XX  
 XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
 PT treating HPV infections.  
 PT  
 XX Disclosure; Page 20-21; 756pp; English.  
 XX  
 XX The present invention describes an isolated prepared human papillomavirus

CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine  
 CC production. Peptides and corresponding nucleic acid compositions from the  
 CC present invention are useful for stimulating an immune response to HPV by  
 CC stimulating the production of CII or HII responses, specifically in the  
 CC treatment or prophylaxis of HPV infection, in persons who have not  
 CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides  
 CC can also be used in a tetramer staining assay to assess peripheral blood  
 CC mononuclear cells for the presence of antigen-specific CTLs following  
 CC exposure to a pathogen or immunogen, and as reagents to evaluate immune  
 CC recall responses or evaluate the efficacy of a vaccine. The vaccine  
 CC compositions are useful for removing warts or treating HPV infections.  
 CC The epitopes for inclusion in an epitope-base vaccine may be selected  
 CC from conserved regions of viral or tumour-associated antigens, which  
 CC reduces the likelihood of escape mutants, also immunosuppressive epitopes  
 CC that may be present in whole antigens can be avoided with the use of  
 CC epitope-base vaccines. An additional advantage is the ability to combine  
 CC selected epitopes (CTL and HTL) and to modify the composition of the  
 CC epitopes achieving enhanced immunogenicity, the major benefit of the  
 CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent  
 CC polypeptide sequences used in the exemplification of the present  
 CC invention  
 XX  
 XX Sequence 158 AA;  
 SQ

Query Match 100.0%; Score 125; DB 4; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 RDGNPYAVCDKCLKFYISKISEY 22  
 DB 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 8  
 ADF09515  
 ID ADF09515 standard; protein; 158 AA.  
 XX  
 XX ADF09515;  
 XX  
 XX 12-FEB-2004 (first entry)  
 XX  
 XX Human papillomavirus 16 E6 SEQ ID NO:16.  
 DE  
 XX human; protein-protein interaction; virucide; cytostatic; vaccine;  
 KW human papilloma virus; HPV; cancer.  
 XX  
 XX Human papillomavirus.  
 OS  
 XX WO2003068940-A2.  
 XX  
 XX 21-AUG-2003.  
 XX  
 XX 14-FEB-2003; 2003WO-US004594.  
 XX  
 XX 14-FEB-2002; 2002US-0356911P.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 XX (HOFF) HOFFMANN LA ROCHE INC.  
 XX  
 XX Jackson A, Ooi CE, Lewin DA, Cuthill S;  
 PI WPI; 2003-689668/85.  
 XX  
 XX N-PSDB; ADF09607.  
 XX  
 XX New purified complex comprising a first polypeptide and a second  
 PT polypeptide, useful for identifying agents for treating/preventing a  
 PT condition involving altered level of the complex e.g. human papilloma  
 XX virus infection, or cancer.  
 XX  
 XX Example 3; SEQ ID NO 16; 156pp; English.  
 XX  
 XX The invention relates to a novel purified complex comprising a first  
 CC polypeptide and a second polypeptide, where the polypeptides comprise

CC defined amino acid sequences listed in the specification, and where the  
 CC first polypeptide binds to the second polypeptide. A complex of the  
 CC invention has virucide and cytostatic activity, and may have a use as a  
 CC vaccine. The complex is useful for identifying agents for treating or  
 CC preventing a conditions involving altered level of the complex. e.g.  
 CC human papilloma virus (HPV) infection, or cancer. The compositions,  
 CC antibodies, vectors and methods are useful for treating such diseases.  
 CC The sequences shown in ADF09500-ADF09583 represent proteins of the  
 CC invention.

CC Sequence 158 AA;  
 SQ Query Match 100.0%; Score 125; DB 7; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
 DB 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 9  
 ADL90078  
 ID ADL90078 standard; protein; 158 AA.  
 AC ADL90078;  
 XX 17-JUN-2004 (first entry)  
 DT Human papillomavirus 16-E6 protein, SEQ ID 18.  
 DE Immune response; immunoglobulin; Ig; E6.  
 KW Human papillomavirus.  
 OS WO2004027049-A2.  
 XX 01-APR-2004.  
 XX 18-SEP-2003; 2003WO-US030188.  
 XX 20-SEP-2002; 2002US-0412219P.  
 PR 14-MAR-2003; 2003WO-US007995.  
 XX (ASTR-) ASTRAL INC.  
 PA Bot A, Wang L, Smith D, Phillips B;  
 FI WP1; 2004-295415/27.  
 DR Generating an immune response to an antigen, useful for generating  
 PT desired T cell responses comprising administering an immunoglobulin having  
 PT one peptide epitope of the antigen attached to the immunoglobulin.  
 XX Disclosure; Fig 1G; 154pp; English.  
 XX The present invention relates to a method for generating an immune  
 CC response to an antigen in a patient. The method comprises administering  
 CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at  
 CC least one peptide epitope of the antigen attached to the Ig or its  
 CC portion and administering the immunoglobulin or its portion in  
 CC conjunction with a RNA segment. The present sequence is an antigen  
 CC sequence, used to illustrate the invention.

CC Sequence 158 AA;  
 SQ Query Match 100.0%; Score 125; DB 8; Length 158;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
 DB 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 10  
 AAW35741  
 ID AAW35741 standard; protein; 162 AA.  
 XX AAW35741;  
 AC 25-MAR-2003 (revised)  
 DT 16-FEB-1998 (first entry)  
 XX Human papillomavirus type 16 E6 protein.  
 DE Complete genome; circular; human papillomavirus type 16; HPV16 E6;  
 KW cervical dysplasia; cervical cancer; cervical smear.  
 OS Human papillomavirus type 16.  
 XX Key Location/Qualifiers  
 FH Misc-difference 90  
 FT Misc-difference 159  
 FT Misc-difference 159  
 FT /note= "End of protein sequence even though 3 amino acid  
 residues are given following on"  
 XX US5679509-A.  
 PN 21-OCT-1997.  
 XX 30-SEP-1994; 94US-00316239.  
 XX 28-SEP-1993; 93US-00127906.  
 XX (UYNE-) UNIV NEW MEXICO STATE.  
 XX Wheeler CM, Parmenter CA;  
 XX WPI; 1997-525714/48.  
 DR N-PSDB; AAT94723.  
 XX Evaluating risk of cervical dysplasia or cervical cancer - by detecting  
 PT variant form of human papilloma virus 16.  
 XX Claim 7; Col 23-24; 33pp; English.  
 XX Methods have been developed for distinguishing a subset of human  
 CC papilloma virus (HPV) that is associated with an increased risk of  
 CC developing cervical dysplasia or cervical cancer. The methods involve:  
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the  
 CC sample and determining if the base at position 350 of the E6 gene (see  
 CC AAT94723 and AAT94724 for comparison) is T or G, where the presence of G  
 CC at position 350 is associated with an increased risk of developing  
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical  
 CC sample to expose any HPV-16 E6 protein in the sample and determining if  
 CC the amino acid at position 83 of the protein (see position 90 in AAW35741  
 CC and AAW35742 for comparison) is Val or Leu, where the presence of Val at  
 CC position 83 that is associated with an increased risk of developing  
 CC cervical dysplasia or cervical cancer. The present sequence represents  
 CC the reference protein sequence for HPV-16 E6. The 350G variant correlates  
 CC well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4  
 CC for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III;  
 CC 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)  
 XX Sequence 162 AA;  
 SQ Query Match 100.0%; Score 125; DB 2; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYISKISEY 22  
 DB 62 RDGNPYAVCDKCLKFYISKISEY 83

RESULT 11  
AAW35742  
ID AAW35742 standard; protein; 162 AA.  
XX AC AAW35742;  
XX AC AAW35742;  
DT 25-MAR-2003 (revised)  
DT 16-FEB-1998 (first entry)  
XX Human papillomavirus type 16 E6 protein variant.  
DE Complete genome; circular; human papillomavirus type 16; HPV16 E6;  
KW cervical dysplasia; cervical cancer; cervical smear.  
XX Human papillomavirus type 16.  
OS  
XX Key Location/Qualifiers  
FH Misc-difference 90  
FT /note= "Mutated from Leu in the reference sequence  
FT (AAW35741)"  
FT Misc-difference 159  
FT /note= "End of protein sequence even though 3 amino acid  
FT residues are given following on"  
XX US5679509-A.  
XX 21-OCT-1997.  
XX 30-SEP-1994; 94US-00316239.  
XX 28-SEP-1993; 93US-00127906.  
XX (UYNF-) UNIV NEW MEXICO STATE.  
XX Wheeler CM, Parmenter CA;  
XX WPI; 1997-525714/48.  
XX N-PSDB; AAT94742.  
XX Evaluating risk of cervical dysplasia or cervical cancer - by detecting  
XX variant form of human papilloma virus 16.  
XX Claim 7; Col 23-26; 33pp; English.  
XX Methods have been developed for distinguishing a subset of human  
XX papilloma virus (HPV) that is associated with an increased risk of  
XX developing cervical dysplasia or cervical cancer. The methods involve:  
XX (1) preparing a cervical sample to expose any HPV-16 E6 gene in the  
XX sample and determining if the base at position 350 of the E6 gene (see  
XX AAT94723 and AAT94724 for comparison) is T or G, where the presence of G  
XX at position 350 is associated with an increased risk of developing  
XX cervical dysplasia or cervical cancer; and (2) preparing a cervical  
XX sample to expose any HPV-16 E6 protein in the sample and determining if  
XX the amino acid at position 83 of the protein (see position 90 in AAW35741  
XX and AAW35742 for comparison) is Val or Leu, where the presence of Val at  
XX position 83 that is associated with an increased risk of developing  
XX cervical dysplasia or cervical cancer. The present sequence represents  
XX the variant protein sequence for HPV-16 E6. The 350G variant correlates  
XX well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4  
XX for negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III;  
XX 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)  
XX Sequence 162 AA;  
Query Match 100.0%; Score 125; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 1.4e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RDGNPVAVCDKCLKFYISKISEY 22  
DB 62 RDGNPVAVCDKCLKFYISKISEY 83

RESULT 12  
AAO22922  
ID AAO22922 standard; protein; 171 AA.  
XX AC AAO22922;  
XX AC AAO22922;  
DT 12-DEC-2002 (first entry)  
XX Human papillomavirus-16 (HPV16) E6T-protein sequence.  
DE Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;  
KW fusion partner; immunogenicity; HPV infection; neoplasm; HPV16;  
KW human papillomavirus-16; E6T-sequence.  
XX Human papillomavirus.  
OS  
XX EPI243655-A1.  
XX 25-SEP-2002.  
XX 23-MAR-2001; 2001EP-00107271.  
XX 23-MAR-2001; 2001EP-00107271.  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
XX Cid-Arregui A, Zur Hausen H;  
XX WPI; 2002-724952/79.  
XX N-PSDB; AAL53420.  
XX A new DNA sequence encoding a fusion protein comprising a mutagenized HPV  
XX (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a  
XX highly immunogenic fusion partner is useful to vaccinate against HPV  
XX infection.  
XX Disclosure; Fig 2; 34pp; English.  
XX The invention relates to a new DNA sequence encodes an E6 or E7 fusion  
XX protein of HPV, where at least 20% of the original codons are replaced by  
XX codons which lead to enhanced translation in a mammalian cell, containing  
XX a mutation which results in production of a truncated non-functional  
XX protein, and encoding a highly immunogenic polypeptide fusion partner  
XX capable of enhancing immunogenicity of the E6 or E7 protein in the  
XX mammalian host. The invention is used as a vaccine for the prevention or  
XX treatment of an HPV infection or a neoplasm associated with HPV  
XX infection. This sequence represents the human papillomavirus-16 (HPV16)  
XX E6T-protein sequence of the invention.  
XX Sequence 171 AA;  
Query Match 100.0%; Score 125; DB 5; Length 171;  
Best Local Similarity 100.0%; Pred. No. 1.5e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 RDGNPVAVCDKCLKFYISKISEY 22  
DB 67 RDGNPVAVCDKCLKFYISKISEY 88  
RESULT 13  
AAR97563  
ID AAR97563 standard; protein; 172 AA.  
XX AC AAR97563;  
XX 27-AUG-2003 (revised)  
DT 11-JAN-1997 (first entry)  
XX Human papilloma virus E6/E7 protein variant.  
DE Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;  
KW Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;

KW humoral immune response; cellular immune response; vaccine.  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO9619496-A1.  
 XX  
 XX 27-JUN-1996.  
 PD  
 XX 20-DEC-1995; 95WO-AU0000868.  
 PF  
 XX 20-DEC-1994; 94AU-00000157.  
 PR  
 XX (CSLC-) CSL LTD  
 PA (UYQU ) UNIV QUEENSLAND.  
 PA  
 XX Edwards SJ, Cox J, Webb EA, Frazer I;  
 PI WPI; 1996-309518/31.  
 XX N-PSDB; AAT31835.  
 DR  
 XX Vaccine variants of human papilloma virus antigens - contain variants of  
 PT E6 and/or E7 protein, pref. deletion mutants, and are used to treat or  
 PT prevent HPV infection.  
 XX  
 XX Example 3; Page 18; 37pp; English.  
 PS  
 XX A variant of the human papilloma virus (HPV) E6 or E7 protein which  
 CC elicits a humoral and/or cellular immune response against HPV can be used  
 CC in vaccines against HPV or to treat HPV infection. The variant is  
 CC preferably a deletion mutant comprising at least half, and preferably two  
 CC -thirds of full length E6 or E7 protein starting from the N- or C-  
 CC terminal, or is a full length E6 moiety fused to a full length E7 moiety.  
 CC The variant optionally has a linkage moiety and a foreign protein or  
 CC peptide which facilitates the purification of, and enhances the  
 CC immunogenicity of, the fusion protein. This sequence is a fusion protein  
 CC of the C-terminal end of E7 and the N-terminal end of E6. (Updated on 27-  
 CC AUG-2003 to correct OS field.)  
 XX  
 SQ Sequence 172 AA;  
 Query Match 100.0%; Score 125; DB 2; Length 172;  
 Best Local Similarity 100.0%; Pred. NO. 1.5e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RDGNPYAVCDKCLFYISKISEY 22  
 DB 131 RDGNPYAVCDKCLFYISKISEY 152  
 RESULT 14  
 ADF31985  
 ID ADF31985 standard; protein; 180 AA.  
 AC  
 AC ADF31985;  
 XX  
 XX 12-FEB-2004 (first entry)  
 DT  
 XX Human papillomavirus fusion gene.  
 DE  
 XX human papillomavirus; cervix cancer.  
 KW  
 XX Homo sapiens.  
 OS  
 XX CN1381583-A.  
 PN  
 XX 27-NOV-2002.  
 PD  
 XX 24-APR-2002; 2002CN-00117143.  
 PF  
 XX 24-APR-2002; 2002CN-00117143.  
 PR  
 XX (ONCO-) INST ONCOLOGY TUMOR HOSPITAL CHINESE ACA.  
 PA  
 XX

PI Zhao Q;  
 XX  
 XX WPI; 2003-258260/26.  
 DR N-PSDB; ADF31984.  
 XX  
 XX Human papillomavirus E6/E7 fusion gene and its efficient expression  
 PT carrier and fusion protein vaccine.  
 PT  
 XX Claim 8; SEQ ID NO 2; 16pp; Chinese.  
 PS  
 XX The present invention relates to human papillomavirus E6/E7 fusion gene,  
 CC its preparing process, the process for configuring the efficient  
 CC expression carrier containing the gene and resultant expression carrier,  
 CC the fusion protein prepared from the gene, and the application of the  
 CC fusion gene and expression protein to medical science and medicine to  
 CC treat cervix cancer are disclosed. The present sequence represents the  
 CC human papillomavirus fusion gene.  
 XX  
 SQ Sequence 180 AA;  
 Query Match 100.0%; Score 125; DB 7; Length 180;  
 Best Local Similarity 100.0%; Pred. NO. 1.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 RDGNPYAVCDKCLFYISKISEY 22  
 DB 62 RDGNPYAVCDKCLFYISKISEY 83  
 RESULT 15  
 AAR63865  
 ID AAR63865 standard; protein; 188 AA.  
 XX  
 AC AAR63865;  
 XX  
 DT 16-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 28-JUN-1995 (first entry)  
 XX  
 DE HPV16 E6/E7 proteins.  
 XX  
 XX HPV; HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia;  
 KW cervix cancer.  
 XX  
 OS Human papillomavirus; strain 16.  
 XX  
 XX Key Location/Qualifiers  
 FT Protein 1..158  
 FT /label= E6\_protein  
 FT 159..188  
 FT /label= E7\_protein  
 FT  
 XX WO9426934-A2.  
 PN  
 XX 24-NOV-1994.  
 PD  
 XX 06-MAY-1994; 94WO-US005085.  
 PF  
 XX 06-MAY-1993; 93US-00058920.  
 PR  
 XX (BAXT ) BAXTER DIAGNOSTICS INC.  
 PA  
 XX Brown JT;  
 PI  
 XX WPI; 1995-006821/01.  
 DR P-PSDB; AAQ75470.  
 DR  
 XX Human papilloma virus detection assay - by amplification using self  
 PT sustained sequence replication and hybridisation with a detector probe.  
 XX  
 XX Disclosure; Page 24-26; 79pp; English.  
 PS  
 XX The sequences of the E6 and E7 polypeptide-encoding regions of human  
 CC

CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded  
 CC proteins in AAR63865-66, respectively. Probes and primers based on these  
 CC sequences were used for HPV infection diagnosis; expression of E6 and E7  
 CC is diagnostic for cervical cancer or pre-malignant states. (Updated on  
 CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise  
 CC OS field)

XX

SQ Sequence 188 AA;

Query Match 100.0%; Score 125; DB 2; Length 188;  
 Best Local Similarity 100.0%; Pred. NO. 1.6e-11;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RDGNPYAVCDKCLKFYKISEY 22  
 |||||  
 Db 62 RDGNPYAVCDKCLKFYKISEY 83

Search completed: November 22, 2004, 20:27:27  
 Job time : 115.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:14:12 ; Search time 113.5 Seconds  
(without alignments)  
69.533 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCDFGSRIRLRHYSVSYVD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	22	8	ADI34604 HPV 18 E6
2	111	92.5	32	2	AAR14751 Seroreact
3	111	92.5	158	2	AAR63866 HPV18 E6/
4	111	92.5	158	2	AAR79656 HPV-18 E6
5	111	92.5	158	2	AAY39968 HPV-18 E6
6	111	92.5	158	3	AAB03176 HPV-18 E6
7	111	92.5	158	4	AAB98427 Human pap
8	111	92.5	158	8	ADL90077 Human pap
9	111	92.5	158	8	ADL90077 Amino aci
10	111	92.5	172	5	AAO22924 Human pap
11	111	92.5	271	5	AAR27728 HPV 18 E6
12	111	92.5	278	2	AAY25385 HPV fusio
13	111	92.5	278	2	AAY02641 Prot.D1/3
14	111	92.5	383	2	AAY25386 HPV fusio
15	111	92.5	383	2	AAY02642 Prot.D1/3
16	96	80.0	158	4	AAB98440 Human pap
17	96	80.0	158	8	ADL90077 Amino aci
18	86	71.7	160	8	ADO44079 Amino aci
19	75	62.8	158	8	ADO44078 Amino aci
20	71	59.2	158	8	ADO44085 Amino aci
21	68	56.7	151	6	AAO22640 HPV-16 pr
22	68	56.7	151	6	AAO22636 HPV prote
23	68	56.7	151	8	ADO44072 Amino aci
24	68	56.7	162	2	AAW35742 Human pap
25	68	56.7	248	8	ADO44062 Amino aci

26	68	56.7	248	8	ADO44064 Amino aci
27	68	56.7	248	8	ADO44060 Amino aci
28	68	56.7	248	8	ADO44066 Amino aci
29	68	56.7	248	8	ADO44068 Amino aci
30	68	56.7	248	8	ADO44070 Amino aci
31	65	54.2	151	8	ADO44080 Amino aci
32	65	54.2	151	8	AAO22766 HPV E6 pe
33	65	54.2	158	3	AAV82462 Human pap
34	65	54.2	158	4	AAB98420 Human pap
35	65	54.2	158	7	ADF09515 Human pap
36	65	54.2	162	2	AAW35741 Human pap
37	65	54.2	171	5	AAO22922 Human pap
38	65	54.2	172	2	AAR97562 Human pap
39	65	54.2	172	2	AAR97563 Human pap
40	65	54.2	180	7	ADF31985 Human pap
41	65	54.2	188	2	AAR63865 HPV16 E6/
42	65	54.2	243	2	AAW99369 Papilloma
43	65	54.2	263	2	AAR27725 HPV 16 B6
44	65	54.2	266	2	AAR97561 Human pap
45	65	54.2	273	2	AAV25376 HPV fusio

## ALIGNMENTS

RESULT 1  
ADI34604  
ID ADI34604 standard; peptide; 22 AA.  
XX  
AC ADI34604;  
XX  
DT 22-APR-2004 (first entry)  
XX  
DE HPV 18 E6 early coding region derived peptide.  
XX  
KW HPV; E2; E6; E7; cancer, cellular abnormality.  
XX  
OS Human papillomavirus.  
XX  
PN WO2004005469-A2.  
XX  
PD 15-JAN-2004.  
XX  
PF 02-JUL-2003; 2003WO-US020887.  
XX  
PR 02-JUL-2002; 2002US-0394172P.  
PR 01-JUL-2003; 2003US-00612818.  
XX  
(IMPA-) IMPACT DIAGNOSTICS INC.  
PA Hu YX, Rosenfeld MJ;  
PI WPI; 2004-142978/14.  
XX  
PT New peptides from the E2, E6 or E7 proteins of human papillomavirus (HPV)  
PT 16 or 18, useful for detecting and/or diagnosing HPV-associated cellular  
PT abnormalities or cervical dysplasia or carcinoma.  
PS Claim 4; SEQ ID NO 5; 31pp; English.  
PS  
CC The invention relates to an isolated protein sequence or peptide from the  
CC E2, E6 or E7 early coding region of human papillomavirus (HPV) that is  
CC soluble in an aqueous medium, and characterized by a relative abundance of  
CC tryptophan, methionine and cysteine residues, and a relative abundance of  
CC glycine and asparagine residues. The protein sequences can be used in a  
CC method for detecting or diagnosing cancer or cellular abnormalities. The  
CC method involves reacting a sample of body fluid or tissue likely to  
CC contain antibodies with one or more protein sequences or peptides cited  
CC above, forming an antibody-peptide complex comprising at least one of the  
CC protein sequences or peptides and the sample antibodies, and detecting  
CC the antibody-peptide complex. The protein sequences and method are useful  
CC for detecting and/or diagnosing HPV-associated epithelial cell  
CC abnormalities, precancerous conditions and cancers, such as cervical

CC cellular abnormalities selected from kollocytosis, hyperkeratosis,  
 CC precancerous conditions encompassing intraepithelial lesions, high-grade  
 CC dysplasias, invasive cancers and malignant cancers. The present sequence  
 CC represents a specific example of a peptide derived from HPV 18 E6 early  
 CC coding region.

XX  
 SQ Sequence 22 AA;  
 Query Match 100.0%; Score 120; DB 8; Length 22;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-12;  
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KCIDFGSRIRRLRHYSVSDVYGD 22  
 |||||  
 DB 1 KCIDFGSRIRRLRHYSVSDVYGD 22

RESULT 2  
 AAR14751  
 ID AAR14751 standard; protein; 32 AA.

XX  
 AC AAR14751;  
 DT 28-JAN-1992 (first entry)

XX Seroreactive epitope #3 of HPV 18 protein E6.

DE vaccine; HPV18.

XX Synthetic.

XX EP456197-A.

XX 13-NOV-1991.

XX 07-MAY-1991; 91EP-00107423.

XX 10-MAY-1990; 90DE-04015044.

XX (BEHW ) BEHRINGWERKE AG.

XX Bleul C, Gissmann L, Muller M;

XX WPI; 1991-334182/46.

XX New sero-reactive epitope(s) of human papilloma virus 18 proteins - and  
 PT corresp. proteins and antibodies, useful in vaccines and for diagnosis.

XX Claim 2; Page 5; 8pp; German.

CC This peptide can be used to identify antibodies specific to E6 protein.  
 CC It is also useful for a vaccine against HPV18. The E6 epitope was  
 CC identified using anti-E6 serum to screen a recombinant phage expression  
 CC library containing 100bp fragments of HPV18 DNA. The DNA inserts from  
 CC positive phage were sequenced and based on this information, overlapping  
 CC decapeptides were prepared on polyethylene pins. They were tested (ELISA)  
 CC against the antisera to locate the epitopes. See AAR14748-R14753

XX Sequence 32 AA;

Query Match 92.5%; Score 111; DB 2; Length 32;  
 Best Local Similarity 95.5%; Pred. No. 7.7e-11;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KCIDFGSRIRRLRHYSVSDVYGD 22  
 |||||  
 DB 5 KCIDFYSRIRRLRHYSVSDVYGD 26

RESULT 3  
 AAR63866  
 ID AAR63866 standard; protein; 158 AA.

AC AAR63866;  
 DT 16-OCT-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 28-JUN-1995 (first entry)

XX HPV18 E6/E7 proteins.

XX HPV; HPV18; E6 protein; E7 protein; diagnosis; cervical dysplasia;  
 KW cervix cancer.

XX Human papillomavirus; strain 18.

OS WO9426934-A2.

XX 24-NOV-1994.

XX 06-MAY-1994; 94WO-US005085.

XX 06-MAY-1993; 93US-00058920.

XX (BAXT ) BAXTER DIAGNOSTICS INC.

XX Brown JT;

XX WPI; 1995-006821/01.

DR P-PSDE; AAQ75471.

XX Human papilloma virus detection assay - by amplification using self  
 PT sustained sequence replication and hybridisation with a detector probe.

XX Disclosure; Page 27-28; 79pp; English.

XX The sequences of the E6 and E7 polypeptide-encoding regions of human  
 CC papillomavirus (HPV) 16 and 18 are given in AAQ75470-71 and the encoded  
 CC proteins in AAR63865-66, respectively. Probes and primers based on these  
 CC sequences were used for HPV infection diagnosis; expression of E6 and E7  
 CC is diagnostic for cervical cancer or pre-malignant states. (Updated on  
 CC 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standardise  
 CC OS field)

XX Sequence 158 AA;

Query Match 92.5%; Score 111; DB 2; Length 158;  
 Best Local Similarity 95.5%; Pred. No. 4.6e-10;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 KCIDFGSRIRRLRHYSVSDVYGD 22  
 |||||  
 DB 67 KCIDFYSRIRRLRHYSVSDVYGD 88

RESULT 4

AAR79656

ID AAR79656 standard; protein; 158 AA.

XX AAR79656;

XX 25-MAR-2003 (revised)

DT 06-DEC-1995 (first entry)

XX HPV-18 E6 protein.

XX Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell cycle;  
 KW cell proliferation; cancer; psoriasis; fibrosis.

XX Homo sapiens.

XX WO9518974-A2.

XX 13-JUL-1995.

XX 04-JAN-1995; 95WO-US000164.



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XX 04-JAN-1994; 94US-00176937.
XX 23-MAY-1994; 94US-00247904.
XX 27-MAY-1994; 94US-00250795.
XX 13-SEP-1994; 94US-00305520.
XX (MITO-) MITOTIX INC.
XX PA
XX PI Draetta G, Rolfe M, Eckstein JW, Cottarel G, Gyuris J;
XX DR N-PSDB; AAQ97848.
XX DR WPI; 1995-255137/33.
XX PT Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle
XX PT regulatory proteins - also new ubiquitin conjugating enzymes, their
XX PT related nucleic acid, vectors, antibodies etc., useful for regulating
XX PT e.g. cell proliferation.
XX PS Disclosure; Page 100-101; 157pp; English.
XX CC HPV-18 E6 cDNA (given in AAQ97848) was amplified from a HeLa cell cDNA
XX CC library using the primers given in AAQ97846-47. The gene was subcloned
XX CC into a baculovirus vector for expression of recombinant E6 in Sf9 insect
XX CC cells for use as a component of an in vitro ubiquitin conjugating system.
XX CC (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 158 AA;
Query Match 92.5%; Score 111; DB 2; Length 158;
Best Local Similarity 95.5%; Pred. No. 4.6e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KCIDFGSRIRRLHYSDSVYGD 22
Db 67 KCIDFYSRIRRLHYSDSVYGD 88
RESULT 5
AAV39968
ID AAV39968 standard; protein; 158 AA.
XX AC AAV39968;
XX DT 15-DEC-1999 (first entry)
XX DE HPV-18 E6 protein sequence..
XX KW Ubiquitin conjugating enzyme; UbCE; ubiquitin-mediated proteolysis;
XX KW cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis;
XX KW proliferative disorder; cancer; restenosis; tissue connective disorder;
XX KW wound healing; fibrosis disorder; rheumatoid arthritis; scleroderma;
XX KW insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
XX KW diagnosis; therapy; E6.
XX OS Human papillomavirus.
XX PN US5968761-A.
XX FD 19-OCT-1999.
XX PF 07-JUN-1995; 95US-00486663.
XX PR 04-JAN-1994; 94US-00176937.
XX PR 23-MAY-1994; 94US-00247904.
XX PR 27-MAY-1994; 94US-00250795.
XX PR 13-SEP-1994; 94US-00305520.
XX PA (MITO-) MITOTIX INC.
XX PI Chiu MI, Cottarel G, Berlin V, Damagnez V, Draetta G, Rolfe M;
XX DR WPI; 1999-590402/50.
XX DR N-PSDB; AAZ27568.

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```

XX Identifying ubiquitination inhibitors using novel ubiquitin conjugating
XX enzymes.
XX Example 2; Col 89-92; 61pp; English.
XX CC This sequence is the human papillomavirus E6 protein. The invention
XX CC relates to assays for identifying an inhibitor of ubiquitin-mediated
XX CC proteolysis of a cell-cycle regulatory protein comprising contacting a
XX CC candidate agent with an ubiquitin-conjugating system and measuring the
XX CC level of ubiquitination. The ubiquitin-conjugating system comprises: (a)
XX CC a reconstituted protein mixture including a ubiquitin conjugating enzyme
XX CC (UbCE) produced by the expression of a nucleic acid which hybridizes
XX CC under high stringency conditions to human UbCE, Candida albicans UbCE, or
XX CC Schizosaccharomyces pombe UbCE coding sequences; (b) a regulatory protein
XX CC ; and (c) ubiquitin. The polynucleotides are useful for identifying
XX CC ubiquitination inhibitors. The polynucleotides, polypeptides, antisense
XX CC compounds and antibodies against them may also be useful for the
XX CC treatment and/or diagnosis of proliferative disorders (e.g. cancer,
XX CC atherosclerosis, or restenosis), tissue connective disorders, controlling
XX CC wound healing, and disorders characterized by fibrosis (e.g. rheumatoid
XX CC arthritis, insulin dependent diabetes mellitus, glomerulonephritis,
XX CC cirrhosis, and scleroderma)
XX SQ Sequence 158 AA;
Query Match 92.5%; Score 111; DB 2; Length 158;
Best Local Similarity 95.5%; Pred. No. 4.6e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 KCIDFGSRIRRLHYSDSVYGD 22
Db 67 KCIDFYSRIRRLHYSDSVYGD 89
RESULT 6
AAB03176
ID AAB03176 standard; protein; 158 AA.
XX AC AAB03176;
XX DT 12-SEP-2003 (revised)
XX DT 23-OCT-2000 (first entry)
XX DE HPV-18 E6 protein.
XX KW HPV-18 E6; ubiquitin mediated proteolysis; human;
XX KW cellular protein half life; ubiquitination inhibitor; p53; cyclin;
XX KW cell cycle regulator; myc deregulation; human papillomavirus;
XX KW HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia;
XX KW epidermal neoplasia; psoriasis; connective tissue disorder;
XX KW wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic.
XX OS Human papillomavirus; 18.
XX PN US6068982-A.
XX PD 30-MAY-2000.
XX PF 17-DEC-1996; 96US-00767942.
XX PR 04-JAN-1994; 94US-00176937.
XX PR 23-MAY-1994; 94US-00247904.
XX PR 27-MAY-1994; 94US-00250795.
XX PR 13-SEP-1994; 94US-00305520.
XX PR 07-JUN-1995; 95US-00486663.
XX PA (MITO-) MITOTIX INC.
XX PI Chiu MI, Cottarel G, Berlin V, Draetta G, Damagnez V, Rolfe M;
XX DR WPI; 2000-410854/35.
XX DR N-PSDB; AAA61623.

```

XX Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory  
PT protein for treating cancers involves measuring ubiquitination levels of  
PT the protein in the presence of candidate agent in an eukaryotic cell.  
XX  
PS Example 2; Col 97-100; 73pp; English.  
XX  
XX The invention relates to a method of identifying an inhibitor of  
CC ubiquitin-mediated proteolysis of a cell cycle regulatory protein  
CC comprising contacting an engineered eukaryotic cell with a candidate  
CC agent; the eukaryotic cells is engineered to express a recombinant human,  
CC Candida albicans or Schizosaccharomyces pombe ubiquitin- conjugating  
CC enzyme (AAB03169-B03171), a cell cycle regulatory protein (such as p53)  
CC and ubiquitin. The specification also discloses novel Candida albicans  
CC and Schizosaccharomyces pombe ubiquitin-conjugating enzymes, caUBCE and  
CC spUBCE (AAB03170, AAB03171), and two novel human ubiquitin-conjugating  
CC enzymes, huBCE and rapUBC (AAB03169, AAB03173). The ubiquitin-mediated  
CC proteolysis system is the major pathway for the selective, controlled  
CC degradation of intracellular proteins in eukaryotic cells. In particular,  
CC this system controls the half-lives of cellular proteins, and is  
CC important in controlling the levels of proteins involved in cell cycle  
CC progression. Alterations in the ubiquitination of these proteins may  
CC therefore play a role in the development of cancers. For example, human  
CC papillomaviruses such as HPV-18 encode a transforming protein, E6  
CC (AAB03176), which combines with a cellular E6-associated protein (E6-AP;  
CC AAB03177) to stimulate the ubiquitination of p53, thus targeting it for  
CC degradation. The ubiquitination inhibitors identified according to the  
CC method of the invention are useful for treatment of cervical cancers and  
CC connective tissue disorders and for controlling the wound healing  
CC process. They are also useful in treatment of hyperplastic epidermal  
CC conditions such as psoriasis, neoplastic epidermal conditions, skin  
CC cancers e.g., basal cell carcinomas, squamous cell carcinomas. The  
CC inhibitors are useful for deregulating myc expression and rendering the  
CC cells sensitive to chemotherapeutic treatment or to upset the balance of  
CC transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-  
CC mediated degradation of cyclins are useful as antiproliferative agents.  
CC The present sequence represents HPV-18 E6 protein. (Updated on 12-SEP-  
CC 2003 to standardise OS field)  
XX  
SQ Sequence 158 AA;  
  
Query Match 92.5%; Score 111; DB 3; Length 158;  
Best Local Similarity 95.5%; Pred. No. 4.6e-10;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 KCIDFGSRIRLELHYSDSVYGD 22  
||| |||||  
DB 67 KCIDFYSRIRLELHYSDSVYGD 88  
  
RESULT 7  
AAB98427  
ID AAB98427 standard; protein; 158 AA.  
XX  
AC AAB98427;  
XX  
DT 22-AUG-2001 (first entry)  
XX  
DE Human papillomavirus protein HPV18 E6.  
XX  
KW Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV;  
KW epitope; T cell; identification; vaccine; infection; genital wart;  
KW neoplastic growth; antiviral.  
XX  
OS Human papillomavirus.  
XX  
XX WO200141799-A1.  
PN  
XX  
PD 14-JUN-2001.  
XX  
PF 11-DEC-2000; 2000WO-US033549.  
XX  
XX 10-DEC-1999; 99US-0172705P.  
PR

PR 15-AUG-2000; 2000US-00641528.  
XX (EPIM-) EPIMUNE INC.  
XX  
PI Sette A, Sidney J, Southwood S, Chesnut R, Cellis E, Grey HM;  
XX  
XX WPI; 2001-381497/40.  
DR  
XX  
XX An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
PT treating HPV infections.  
PT  
XX Disclosure; Page 22; 756pp; English.  
XX  
XX The present invention describes an isolated prepared human papillomavirus  
CC (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine  
CC production. Peptides and corresponding nucleic acid compositions from the  
CC present invention are useful for stimulating an immune response to HPV by  
CC stimulating the production of CTL or HTL responses, specifically in the  
CC treatment or prophylaxis of HPV infection, in persons who have not  
CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides  
CC can also be used in a tetramer staining assay to assess peripheral blood  
CC mononuclear cells for the presence of antigen-specific CTLs following  
CC exposure to a pathogen or immunogen, and as reagents to evaluate immune  
CC recall responses or evaluate the efficacy of a vaccine. The vaccine  
CC compositions are useful for removing warts or treating HPV infections.  
CC The epitopes for inclusion in an epitope-base vaccine may be selected  
CC from conserved regions of viral or tumour-associated antigens, which  
CC reduces the likelihood of escape mutants, also immunosuppressive epitopes  
CC that may be present in whole antigens can be avoided with the use of  
CC selected epitopes. An additional advantage is the ability to combine  
CC selected epitopes (CTL and HTL) and to modify the composition of the  
CC epitopes achieving enhanced immunogenicity, the major benefit of the  
CC vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent  
CC polypeptide sequences used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 158 AA;  
  
Query Match 92.5%; Score 111; DB 4; Length 158;  
Best Local Similarity 95.5%; Pred. No. 4.6e-10;  
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 KCIDFGSRIRLELHYSDSVYGD 22  
||| |||||  
DB 67 KCIDFYSRIRLELHYSDSVYGD 88  
  
RESULT 8  
ADL90077  
ID ADL90077 standard; protein; 158 AA.  
XX  
AC ADL90077;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human papillomavirus 18-E6 protein, SEQ ID 17.  
XX  
KW Immune response; immunoglobulin; Ig; E6.  
XX  
OS Human papillomavirus.  
XX  
XX WO2004027049-A2.  
FN  
XX  
PD 01-APR-2004.  
XX  
PF 18-SEP-2003; 2003WO-US030188.  
XX  
XX 20-SEP-2002; 2002US-0412219P.  
PR  
XX 14-MAR-2003; 2003WO-US007995.  
XX  
XX (ASTR-) ASTRAL INC.  
XX  
PI Bot A, Wang L, Smith D, Phillips B;

XX WPI; 2004-295415/27.  
 XX Generating an immune response to an antigen, useful for generating  
 PT desired T cell responses comprises administering an immunoglobulin having  
 PT one peptide epitope of the antigen attached to the immunoglobulin.  
 XX  
 XX Disclosure; Fig 1G; 154pp; English.  
 XX  
 CC The present invention relates to a method for generating an immune  
 CC response to an antigen in a patient. The method comprises administering  
 CC to the patient an immunoglobulin (Ig) or its portion where the Ig has at  
 CC least one peptide epitope of the antigen attached to the Ig or its  
 CC portion and administering the immunoglobulin or its portion in  
 CC conjunction with a RNA segment. The present sequence is an antigen  
 CC sequence, used to illustrate the invention.  
 XX  
 XX Sequence 158 AA;  
 SQ  
 Query Match 92.5%; Score 111; DB 8; Length 158;  
 Best Local Similarity 95.5%; Pred. No. 4.6e-10;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1 KCIDFGSRIRRLRHYSVSYGD 22  
 DB 67 KCIDFYSRIRRLRHYSVSYGD 88  
 XX  
 RESULT 9  
 ADO44074  
 ID ADO44074 standard; protein; 158 AA.  
 XX  
 AC ADO44074;  
 XX  
 DT 15-JUL-2004 (first entry)  
 XX  
 DE Amino acid sequence of the E6 polypeptide of HPV18.  
 XX  
 KW E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;  
 KW cervical cancer; immune response; lower gastrointestinal tract cancer;  
 KW anal cancer; reproductive system cancer; penile cancer; vulvar cancer.  
 XX  
 OS Human papillomavirus type 18.  
 XX  
 PN W02004030636-A2.  
 XX  
 PD 15-APR-2004.  
 XX  
 PF 02-OCT-2003; 2003WO-US031726.  
 XX  
 PR 03-OCT-2002; 2002US-0415929P.  
 XX  
 PA (AMHP) WYETH HOLDINGS CORP.  
 XX  
 PI Smith L, Cassetti MC;  
 XX  
 DR WPI; 2004-316328/29.  
 DR N-PSDB; ADO44101.  
 XX  
 PT New polypeptide comprising human papillomavirus E6 and E7 polypeptides,  
 PT useful for treating or preventing human papillomavirus (HPV)-associated  
 PT cancers, e.g. cervical cancer.  
 XX  
 PS Disclosure; Page 78; 101pp; English.  
 XX  
 CC ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses.  
 CC ADO44098 is the consensus sequence derived from these polypeptides. The  
 CC specification describes human papillomavirus E6 and E7 polypeptides,  
 CC where the E7 polypeptide has mutations at any one or more of the amino  
 CC acids corresponding to amino acids 24, 26 or 91 of the sequence given in  
 CC ADO44073 and the E6 polypeptide has no mutations or has mutations at any  
 CC one or more of the amino acids corresponding to amino acids 63 or 106 of  
 CC there sequence given in ADO44072. The polypeptides of the invention are

CC useful for treating or preventing human papillomavirus (HPV)-associated  
 CC cancers, such as cervical cancer. The fusion proteins and nucleic acids  
 CC encoding the fusion proteins are useful for generating immune responses  
 CC against HPV. They are also useful for treating lower gastrointestinal  
 CC tract cancers, e.g. anal cancer, and other cancers of the reproductive  
 CC system, including penile and vulvar cancer.  
 XX  
 XX Sequence 158 AA;  
 SQ  
 Query Match 92.5%; Score 111; DB 8; Length 158;  
 Best Local Similarity 95.5%; Pred. No. 4.6e-10;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX  
 QY 1 KCIDFGSRIRRLRHYSVSYGD 22  
 DB 67 KCIDFYSRIRRLRHYSVSYGD 88  
 XX  
 RESULT 10  
 AAO22924  
 ID AAO22924 standard; protein; 172 AA.  
 XX  
 AC AAO22924;  
 XX  
 DT 12-DEC-2002 (first entry)  
 XX  
 DE Human papillomavirus-18 (HPV18) E6E7-protein sequence.  
 XX  
 KW Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;  
 KW fusion partner; immunogenicity; HPV infection; neoplasm; HPV18;  
 KW human papillomavirus-18; E6E7-sequence.  
 XX  
 OS Human papillomavirus.  
 XX  
 PN EP1243655-A1.  
 XX  
 PD 25-SEP-2002.  
 XX  
 PF 23-MAR-2001; 2001EP-00107271.  
 XX  
 PR 23-MAR-2001; 2001EP-00107271.  
 XX  
 PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
 XX  
 PI Cid-Arregui A, Zur Hausen H;  
 XX  
 DR WPI; 2002-724952/79.  
 DR N-PSDB; AAL53422.  
 XX  
 PT A new DNA sequence encoding a fusion protein comprising a mutagenized HPV  
 PT (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a  
 PT highly immunogenic fusion partner is useful to vaccinate against HPV  
 PT infection.  
 XX  
 PS Disclosure; Fig 4; 34pp; English.  
 XX  
 CC The invention relates to a new DNA sequence encodes an E6 or E7 fusion  
 CC protein of HPV, where at least 20% of the original codons are replaced by  
 CC codons which lead to enhanced translation in a mammalian cell, containing  
 CC a mutation which results in production of a truncated non-functional  
 CC protein, and encoding a highly immunogenic polypeptide fusion partner  
 CC capable of enhancing immunogenicity of the E6 or E7 protein in the  
 CC mammalian host. The invention is used as a vaccine for the prevention or  
 CC treatment of an HPV infection or a neoplasm associated with HPV  
 CC infection. This sequence represents the human papillomavirus-18 (HPV18)  
 CC E6E7-protein sequence of the invention  
 XX  
 XX Sequence 172 AA;  
 SQ  
 Query Match 92.5%; Score 111; DB 5; Length 172;  
 Best Local Similarity 95.5%; Pred. No. 5.1e-10;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSDSVYGD 22  
 |||||  
 Db 73 KCIDFYSRIRRLRHYSDSVYGD 94

## RESULT 11

AAAR27728  
 ID AAR27728 standard; protein; 271 AA.

XX AC AAR27728;  
 XX DT 24-OCT-2003 (revised)  
 XX DT 25-MAR-2003 (revised)  
 XX DT 09-MAR-1993 (first entry)  
 XX XX HPV 18 E6 protein fragment.  
 XX XX Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;  
 XX KW immunotherapeutic.  
 XX OS Human papillomavirus; 18.

XX FH Key Location/Qualifiers  
 XX FT Peptide 2..259  
 XX FT /note= "HPV-18 E6 protein"

XX PN W09216636-A1.

XX XX 01-OCT-1992.

XX PF 10-MAR-1992; 92WO-GB000424.

XX XX 14-MAR-1991; 91GB-00005383.

XX PR (IMMU ) IMMUNOLOGY LTD.

XX PI Boursnell MEG, Inglis SC, Munro AJ;

XX DR WPI; 1992-349219/42.

XX DR N-PSDB; AAQ29390.

XX XX Recombinant virus vectors encoding human papillomavirus proteins - for  
 PT treating and vaccinating against HPV infections and conditions caused by  
 PT them, such as cervical cancer.  
 XX PS Disclosure; Fig 1b; 83pp; English.

XX XX The fragment of DNA contg. the HPV-18 E6/E7 coding region was prepd. by  
 CC PCR from plasmid pBR322/HPV16 (Boshart et al., EMBO J. 3: 1151) using  
 CC oligonucleotides S01 and S02. The prod. of the second reading frame is  
 CC the HPV-18 E7 protein whereas the third reading frame encodes HPV-18 E6.  
 CC The E6 and E7 ORFs are fused together to form a single continuous ORF via  
 CC site directed mutagenesis and the immortalising potential of E7 is  
 CC removed by altering two key codons of the HPV E7 sequence. The single ORF  
 CC of HPV-18 E6/E7 may be inserted into vaccinia virus DNA at neutral sites  
 CC (pref. by inserting two sets of the DNA in opposite orientations to  
 CC overcome the problem of intertypic recombination) to make a recombinant  
 CC virus vector for use immunotherapeutically to activate cells of the  
 CC immune system against HPV. See also AAR27723-43. (Updated on 25-MAR-2003  
 CC to correct FN field.) (Updated on 24-OCT-2003 to standardise OS field)

XX XX Sequence 271 AA;

Query Match 92.5%; Score 111; DB 2; Length 271;

Best Local Similarity 95.5%; Pred. No. 8.5e-10;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSDSVYGD 22

|||||

Db 68 KCIDFYSRIRRLRHYSDSVYGD 89

## RESULT 12

AAAY25385  
 ID AAY25385 standard; protein; 278 AA.

XX AC AAY25385;

XX DT 06-SEP-1999 (first entry)

XX DE HPV fusion protein D1/3-E6-His/HPV18.

XX XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
 XX KW immunological fusion partner; CpG oligonucleotide; immune response;  
 XX KW HPV antigen; prevention; treatment.

XX OS Synthetic.

XX OS Human papillomavirus.

XX PN W09933868-A2.

XX XX 08-JUL-1999.

XX PF 18-DEC-1998; 98WO-EP008563.

XX PR 24-DEC-1997; 97GB-00027262.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Dalemans WLJ, Gerard CMG;

XX DR WPI; 1999-405485/34.

XX DR N-PSDB; AAX78800.

XX PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 PT induce immune response to HPV.

XX XX Example XI; Page 59-60; 62pp; English.

XX CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory CpG  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used for  
 CC preventing or treating HPV induced tumours

XX XX Sequence 278 AA;

Query Match 92.5%; Score 111; DB 2; Length 278;

Best Local Similarity 95.5%; Pred. No. 8.7e-10;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSDSVYGD 22

|||||

Db 178 KCIDFYSRIRRLRHYSDSVYGD 199

## RESULT 13

AAAY02641

ID AAY02641 standard; protein; 278 AA.

XX AC AAY02641;

XX DT 17-OCT-2003 (revised)

XX DT 22-JUN-1999 (first entry)

XX DE Prot.D1/3-E6-His/HPV18 protein.

XX KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;  
 XX KW tumour; lesion; benign; malignant; virus; infection.

XX OS Human papillomavirus.

XX OS Haemophilus influenzae.

XX OS Chimeric.

```

PN WO9910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98WO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX
DR WPI; 1999-190587/16.
DR N-PSDB; AAX29789.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
PS Disclosure; Fig 22; 95pp; English.
XX
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 278 AA;

Query Match 92.5%; Score 111; DB 2; Length 278;
Best Local Similarity 95.5%; Pred. No. 8.7e-10;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLHYSDSVYGD 22
Db 178 KCIDFYSRIRLHYSDSVYGD 199

RESULT 14
AAY25386
ID AAY25386 standard; protein; 383 AA.
XX
AC AAY25386;
XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE Prot.D1/3-E6-E7-His/HPV18 protein.
XX
KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KW tumour; lesion; benign; malignant; virus; infection.
XX
OS Human papillomavirus.
OS Haemophilus influenzae.
OS Chimeric.
XX
PN WO9910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98WO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX
DR WPI; 1999-190587/16.
DR N-PSDB; AAX29790.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
PS Disclosure; Fig 25; 95pp; English.
XX
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 383 AA;

Query Match 92.5%; Score 111; DB 2; Length 383;
Best Local Similarity 95.5%; Pred. No. 1.2e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLHYSDSVYGD 22
Db 178 KCIDFYSRIRLHYSDSVYGD 199

RESULT 15
AAY02642
ID AAY02642 standard; protein; 383 AA.
XX
AC AAY02642;
XX
DT 17-OCT-2003 (revised)
DT 22-JUN-1999 (first entry)
XX
DE Prot.D1/3-E6-E7-His/HPV18 protein.
XX
KW Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KW tumour; lesion; benign; malignant; virus; infection.
XX
OS Human papillomavirus.
OS Haemophilus influenzae.
OS Chimeric.
XX
PN WO9910375-A2.
XX
PD 04-MAR-1999.
XX
PF 17-AUG-1998; 98WO-EP005285.
XX
PR 22-AUG-1997; 97GB-00017953.
XX
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
XX
DR WPI; 1999-190587/16.
DR N-PSDB; AAX29790.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions.
XX
PS Disclosure; Fig 25; 95pp; English.
XX
CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B protein
CC D. The sequence also contains a histidine tag at the C-terminus of the
CC encoded protein. The protein can be used in a vaccine, for immuno-
CC therapeutically treating HPV induced tumour lesions (benign or malignant)
CC and preventing HPV viral infection. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 383 AA;

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Query Match 92.5%; Score 111; DB 2; Length 383;  
 Best Local Similarity 95.5%; Pred No. 1.2e-09;  
 Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRELHYSDSVYGD 22  
 |||||  
 Db 178 KCIDFYSRIRRELHYSDSVYGD 199  
 |||||

Search completed: November 22, 2004, 20:27:28  
 Job time : 114.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:20:21 : Search time 27.5 Seconds  
(without alignments)  
53.054 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDFGSRIRLHRHSDSVVGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap.\*
- 2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap.\*
- 3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap.\*
- 4: /cgn2\_6/ptodata/1/iaa/6B COMB.pap.\*
- 5: /cgn2\_6/ptodata/1/iaa/PTUS COMB.pap.\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	111	92.5	32	1	US-08-466-285-4
2	111	92.5	32	3	US-08-164-768-4
3	111	92.5	158	2	US-08-247-904B-10
4	111	92.5	158	3	US-08-767-942A-19
5	111	92.5	271	1	US-08-117-083-14
6	111	92.5	278	3	US-09-485-885-21
7	111	92.5	383	3	US-09-485-885-23
8	68	56.7	162	1	US-08-316-239B-4
9	65	54.2	158	4	US-09-980-523A-2
10	65	54.2	162	1	US-08-116-239B-3
11	65	54.2	172	3	US-08-860-165-12
12	65	54.2	172	3	US-08-860-165-14
13	65	54.2	172	3	US-09-359-382-12
14	65	54.2	172	3	US-09-359-382-14
15	65	54.2	266	3	US-08-860-165-10
16	65	54.2	266	3	US-09-359-382-10
17	65	54.2	266	4	US-09-367-109A-1
18	65	54.2	273	3	US-09-485-885-4
19	65	54.2	292	3	US-09-485-885-10
20	65	54.2	371	3	US-09-485-885-6
21	65	54.2	371	3	US-09-485-885-14
22	47	39.2	20	3	US-08-159-339A-88
23	47	39.2	20	2	US-08-934-915-44
24	47	39.2	20	2	US-08-934-915-163
25	46.5	38.8	187	3	US-08-737-248-19
26	46	38.3	347	4	US-09-248-796A-15125
27	46	38.3	1313	3	US-08-989-299-9

28 46 38.3 1313 4 US-09-407-427-9 Sequence 9, Appli  
29 45.5 37.9 260 4 US-09-252-991A-23381 Sequence 23381, A  
30 44 36.7 182 1 US-08-117-083-10 Sequence 10, Appl  
31 43.5 36.2 365 4 US-09-134-000C-4931 Sequence 4931, Ap  
32 43.5 36.2 883 4 US-09-489-039A-9716 Sequence 9716, Ap  
33 43 35.8 562 4 US-09-489-039A-12840 Sequence 12840, A  
34 43 35.8 1291 3 US-09-150-460B-10 Sequence 10, Appl  
35 43 35.8 1291 3 US-09-220-641-5 Sequence 5, Appli  
36 42 35.0 107 4 US-09-248-796A-14203 Sequence 14203, A  
37 42 35.0 175 4 US-09-248-796A-20358 Sequence 20358, A  
38 42 35.0 368 3 US-09-000-094-20 Sequence 20, Appl  
39 42 35.0 368 4 US-10-011-749-20 Sequence 20, Appl  
40 42 35.0 368 4 US-09-000-094-20 Sequence 20, Appl  
41 42 35.0 375 3 US-09-000-094-22 Sequence 22, Appl  
42 42 35.0 375 4 US-10-011-749-22 Sequence 22, Appl  
43 42 35.0 375 4 US-09-000-094-22 Sequence 22, Appl  
44 42 35.0 465 3 US-09-000-094-24 Sequence 24, Appl  
45 42 35.0 465 4 US-10-011-749-24 Sequence 24, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-466-285-4

: Sequence 4, Application US/08466285

: Patent No. 5753233

: GENERAL INFORMATION:

: APPLICANT: Bieul, Conrad

: APPLICANT: Gissmann, Lutz

: APPLICANT: Muller, Martin

: TITLE OF INVENTION: Seroreactive Epitopes On Proteins Of

: TITLE OF INVENTION: Human Papillomavirus (HPV)18

: NUMBER OF SEQUENCES: 7

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &

: ADDRESS: Dunner

: STREET: 1300 I Street, N.W., Suite 700

: CITY: Washington

: STATE: D.C.

: COUNTRY: USA

: ZIP: 20005-3315

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent in Release #1.0, Version #1.30

: CURRENT APPLICATION DATA: US/08/466,285

: APPLICATION NUMBER: US/08/466,285

: FILING DATE: 06-JUN-1995

: CLASSIFICATION: 424

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 08/164,768

: FILING DATE: 10-DEC-1993

: CLASSIFICATION: 424

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 07/947,992

: FILING DATE: 21-SEP-1992

: CLASSIFICATION: 424

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: US 07/696,953

: FILING DATE: 08-MAY-1991

: CLASSIFICATION: 424

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: P 40 15 044.5

: FILING DATE: 10-MAY-1990

: CLASSIFICATION: 424

: ATTORNEY/AGENT INFORMATION:

: NAME: Manspeizer, David A.

: REGISTRATION NUMBER: 37,540

: REFERENCE/POCKET NUMBER: 05552.1075-03000

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (202)408-4000





```

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,942A
; FILING DATE: 17-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MIV-029.04
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-767-942A-19

Query Match          92.5%; Score 111; DB 3; Length 158;
Best Local Similarity 95.5%; Pred. No. 1.4e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLHYSDSVYGD 22
Db 67 KCIDFYSRIRLHYSDSVYGD 88

RESULT 5
US-08-117-083-14
; Sequence 14, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Boursnell, Michael E.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 271 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..271

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; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-14

Query Match          92.5%; Score 111; DB 1; Length 271;
Best Local Similarity 95.5%; Pred. No. 2.4e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLHYSDSVYGD 22
Db 68 KCIDFYSRIRLHYSDSVYGD 89

RESULT 6
US-09-485-885-21
; Sequence 21, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21

Query Match          92.5%; Score 111; DB 3; Length 278;
Best Local Similarity 95.5%; Pred. No. 2.5e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLHYSDSVYGD 22
Db 178 KCIDFYSRIRLHYSDSVYGD 199

RESULT 7
US-09-485-885-23
; Sequence 23, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-23

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Query Match 54.2%; Score 65; DB 3; Length 172;

Query Match 54.2%; Score 65; DB 3; Length 172;

Query Match	54.2%	Score 65;	DB 3;	Length 172;
Best Local Similarity	57.1%	Pred. No.	0.018;	

Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLRYHSDSVYG 21  
 ||:|||||:|  
 Db 141 KCLKPYSKISEYRHYCYSLYG 161

RESULT 15  
 US-08-860-165-10  
 ; Sequence 10, Application US/08860165A  
 ; Patent No. 6004557  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EDWARDS, Stirling John  
 ; APPLICANT: COX, John Cooper  
 ; APPLICANT: WEBB, Elizabeth Ann  
 ; APPLICANT: FRAZER, Ian  
 ; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
 ; FILE REFERENCE: 17227/130  
 ; CURRENT APPLICATION NUMBER: US/08/860,165A  
 ; FILING DATE: 1997-09-22  
 ; EARLIER APPLICATION NUMBER: PCT/AU95/00868  
 ; EARLIER FILING DATE: 1995-12-20  
 ; EARLIER APPLICATION NUMBER: AU PN0157  
 ; EARLIER FILING DATE: 1994-12-20  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 10  
 ; LENGTH: 266  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
 US-08-860-165-10

Query Match 54.2%; Score 65; DB 3; Length 266;  
 Best Local Similarity 57.1%; Pred. No. 0.029;  
 Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLRYHSDSVYG 21  
 ||:|||||:|  
 Db 72 KCLKPYSKISEYRHYCYSLYG 92

Search completed: November 22, 2004, 20:33:43  
 Job time : 28.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:19:30 ; Search time 23.5 Seconds  
(without alignments)  
90.075 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDFGSRIRRLRHYSVYGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	92.5	158	1 W6WL18	E6 protein - human
2	96	80.0	158	2 S36551	E6 protein - human
3	75	62.5	158	1 W6WL39	E6 protein - human
4	71	59.2	158	1 W6WLPR	E6 protein - human
5	65	54.2	151	1 W6WL31	E6 protein - human
6	65	54.2	158	1 W6WL58	protein E6 - human
7	64	53.3	149	1 W6WL33	E6 protein - human
8	63	52.5	153	2 S36503	E6 protein - human
9	62	51.7	154	2 S36527	E6 protein - human
10	60	50.0	149	1 W6WL35	E6 protein - human
11	60	50.0	149	1 W6WL58	E6 protein - human
12	59	49.2	148	2 A61237	E6 protein - human
13	59	49.2	148	2 S36545	E6 protein - human
14	59	49.2	148	2 S36573	E6 protein - human
15	58	48.3	150	2 S36544	E6 protein - human
16	57	47.5	149	1 W6WL31	E6 protein - human
17	56	46.7	155	1 W6WL56	E6 protein - human
18	56	46.7	155	2 A44890	E6 protein - human
19	56	46.7	191	1 W6WLRI	E6 protein - rhesu
20	55	45.8	153	1 S15621	E6 protein - human
21	54	45.0	150	1 W6WL42	E6 protein - human
22	54	45.0	159	1 S15614	E6 protein - human
23	54	45.0	159	2 S36497	E6 protein - human
24	51	42.5	211	2 S55153	transcription fact
25	50	41.7	142	2 S36509	E6 protein - human
26	50	41.7	410	2 T3284	hypothetical prote
27	49	40.8	936	2 T34024	hypothetical prote
28	48	40.0	155	1 W6WL43	E6 protein - human
29	47	39.2	190	2 E72748	hypothetical prote

endoglucanase I (E  
prolactin I - chu  
prolactin II - chu  
prolactin precursor  
prolactin precursor  
prolactin - Atlant  
prolactin - Atlant  
prolactin precursor  
prolactin precursor  
laurate omega-hydr  
peptidyl-dipeptida  
probable hydrolase  
probable inositol  
flagellin syntheti  
conserved hypothet  
laurate omega-hydr

30 47 39.2 879 2 A47704  
31 46.5 38.6 187 2 S02304  
32 46.5 38.8 187 2 S06677  
33 46.5 38.8 210 2 I51084  
34 46.5 38.8 210 2 PNO092  
35 46.5 38.8 210 2 A31364  
36 46.5 38.8 210 2 S52475  
37 46.5 38.8 210 2 S34351  
38 46.5 38.8 211 2 S00359  
39 46 38.3 510 1 A34160  
40 46 38.3 1313 1 J02038  
41 45.5 37.9 221 2 H82999  
42 45.5 37.9 1144 2 F84725  
43 45 37.5 88 2 B69623  
44 45 37.5 182 2 E69193  
45 45 37.5 509 1 O4RTLO

RESULT 1  
W6WL18  
E6 protein - human papillomavirus type 18  
C;Species: human papillomavirus type 18  
C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 09-Jul-2004  
A;Accession: A26165; G26251  
R;Seedorf, K.; Oltersdorf, T.; Kraemer, G.; Roewekamp, W.  
EMBO J. 6, 139-144, 1987  
A;Title: Identification of early proteins of the human papilloma viruses type 16 (HPV 16)  
A;Reference number: A91068; MUID:87218459; PMID:3034571  
A;Accession: A26165  
A;Molecule type: DNA  
A;Residues: 1-158 <SEE>  
A;Cross-references: UNIPROT:P06463; GB:X04773; NID:G60876; PIDN:CAA28466.1; PID:G60877  
R;Cole, S.T.; Danos, O.  
J. Mol. Biol. 193, 599-608, 1987  
A;Title: Nucleotide sequence and comparative analysis of the human papillomavirus type 18  
A;Reference number: A92937; MUID:87283882; PMID:3039146  
A;Accession: G26251  
A;Molecule type: DNA  
A;Residues: 1-158 <COL>  
A;Cross-references: GB:X05015; NID:G60975; PIDN:CAA28664.1; PID:G60976  
R;Matlashewski, G.; Banks, L.; Wu-Liao, J.; Spence, P.; Pin, D.; Crawford, L.  
J. Gen. Virol. 67, 1909-1916, 1986  
A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and the p  
A;Reference number: A92791; MUID:86306655; PMID:3018129  
A;Contents: annotation; identification of the protein  
C;Superfamily: papillomavirus E6 protein  
C;Keywords: DNA binding; early protein; transforming protein; zinc finger  
F;32-68/Region: zinc finger CCCC motif  
F;105-141/Region: zinc finger CCCC motif

Query Match 92.5%; Score 111; DB 1; Length 158;

Best Local Similarity 95.5%; Pred. No. 1e-09;

Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRRLRHYSVYGD 22

DB 67 KCIDFGSRIRRLRHYSVYGD 88

#### RESULT 2

S36561

E6 protein - human papillomavirus type 45

C;Species: human papillomavirus type 45

C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004

C;Accession: S36561

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.

A;Reference number: S36469

A;Accession: S36561

```

A:Molecule type: DNA
A:Residues: 1-158 <DEL>
A:Cross-references: UNIPROT:P21735; EMBL:X74479; NID:G397022; PIDN:CAA52573.1; PID:G3970
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match      80.0%; Score 96; DB 2; Length 158;
Best Local Similarity 81.8%; Pred. No. 2.1e-07;
Matches 18; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      1 KCIDFGSRIRLHRHYSVYGD 22
DB      67 KCIDFYSRIRLHRYSNYSYGE 88

RESULT 3
W6WL39
E6 protein - human papillomavirus type 39
C:Species: human papillomavirus type 39
A:Note: host Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: A38502
R:Volpers, C.; Streeseck, R.E.
Virology 181, 419-423, 1991
A:Title: Genome organization and nucleotide sequence of human papillomavirus type 39.
A:Reference number: A38502; MUID:91135017; PMID:1847266
A:Accession: A38502
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <VOL>
A:Cross-references: UNIPROT:P24835; GB:M62849; EMBL:M38185; NID:G333245; PIDN:AAA47050.1
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; transforming protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match      62.5%; Score 75; DB 1; Length 158;
Best Local Similarity 73.7%; Pred. No. 0.00037;
Matches 14; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      2 CIDFGSRIRLHRHYSVY 20
DB      68 CIKFYAKIRLRYSDSVY 86

RESULT 4
W6WLPR
E6 protein - human papillomavirus type ME180 (provirus)
C:Species: human papillomavirus type ME180
A:Note: host Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: C40509
R:Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A:Title: Characterization of a novel human papillomavirus DNA in the cervical carcinoma
A:Reference number: A40509; MUID:91374616; PMID:1716694
A:Accession: C40509
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-158 <REU>
A:Cross-references: UNIPROT:P7962; GB:M73259
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:32-68/Region: zinc finger CCCC motif
F:105-141/Region: zinc finger CCCC motif

Query Match      59.2%; Score 71; DB 1; Length 158;
Best Local Similarity 68.4%; Pred. No. 0.0015;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 CIDFGSRIRLHRHYSVY 20
DB      68 CIKFYAKIRLRYSDSVY 86

```

```

RESULT 5
W6WL51
E6 protein - human papillomavirus type 51
C:Species: human papillomavirus type 51
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C:Accession: E40415
R:Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A:Title: Biologic properties and nucleotide sequence analysis of human papillomavirus type
A:Reference number: A40415; MUID:91303675; PMID:1849326
A:Accession: E40415
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-151 <LUN>
A:Cross-references: UNIPROT:P26554; GB:M62877
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

Query Match      54.2%; Score 65; DB 1; Length 151;
Best Local Similarity 61.9%; Pred. No. 0.012;
Matches 13; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 KCIDFGSRIRLHRHYSVY 21
DB      65 QCLLFYSKIREYRRYSRVY 85

RESULT 6
W6WLHS
Protein E6 - human papillomavirus type 16
C:Species: human papillomavirus type 16
C:Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C:Accession: A03682; T10427
R:Ssedoff, K.; Krammer, G.; Durst, M.; Suhai, S.; Rowekamp, W.G.
Virology 145, 181-185, 1985
A:Title: Human papillomavirus type 16 DNA sequence.
A:Reference number: A22355; MUID:85246220; PMID:2590099
A:Accession: A03682
A:Molecule type: DNA
A:Residues: 1-158 <SEE>
A:Cross-references: UNIPROT:P03126; GB:K02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.S.
J. Virol. 65, 2093-2097, 1991
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the level
A:Reference number: 217014; MUID:91162763; PMID:1848319
A:Accession: T10427
A:Status: preliminary; translated from GB/EMBL/DD5J
A:Molecule type: DNA
A:Residues: 1-158 <KEN>
A:Cross-references: EMBL:X02718; NID:G333031; PIDN:AAA46939.1; PID:G333032
C:Genetics:
A:Gene: E6
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:37-73/Region: zinc finger CCCC motif
F:110-146/Region: zinc finger CCCC motif

Query Match      54.2%; Score 65; DB 1; Length 158;
Best Local Similarity 57.1%; Pred. No. 0.013;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 KCIDFGSRIRLHRHYSVY 21
DB      72 KCLFYSKIREYRRHYSVY 92

RESULT 7
W6WL33

```

QY 2 CIDFGSRIRELRHYSVSYG 21  
| : | : | : | : | : | :  
Db 70 CLLFYSKVRKLRYNCSVYG 89

RESULT 10  
W6WLJ35  
E6 protein - human papillomavirus type 35  
C/Species: human papillomavirus type 35  
A/Note: host Homo sapiens (man)  
C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
C/Accession: E40824; S36521  
R/Marich, J.E.; Pontslar, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.  
Virolgy 186, 770-776, 1992  
A/Rittle: The phylogenetic relationship and complete nucleotide sequence of human papilloma-  
virus type 35  
A/Reference number: A40824; MUID:92124753; PMID:1310198  
A/Accession: E40824  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-149 <MAR>  
A/Cross-references: UNIPROT:P27228; GB:M74117; NID:g333050; PIDN:AAA46966.1; PID:g333051  
R/Dellus, H.; Hofmann, B.  
Submitted to the EMBL Data Library, August 1993  
A/Description: Primer-directed sequencing of human papillomavirus types.  
A/Reference number: S36469  
A/Accession: S36521  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-149 <DEL>  
A/Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998  
A/Experimental source: strain 35H  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; zinc finger  
F:30-66/Region: zinc finger CCCC motif  
F:103-139/Region: zinc finger CCCC motif

Query Match 50.0%; Score 60; DB 1; Length 149;  
Best Local Similarity 54.5%; Pred.No. 0.072;  
Matches 12; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRELRHYSVSYGD 22  
| : | : | : | : | : | :  
Db 65 KCLFPYSKISEYRWYRSVYGE 86

RESULT 11  
W6WL58  
E6 protein - human papillomavirus type 58  
C/Species: human papillomavirus type 58  
A/Note: host Homo sapiens (man)  
C/Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: E36779  
R/Kiriri, Y.; Iwamoto, S.; Matsukura, T.  
Virolgy 185, 424-427, 1991  
A/Rittle: Human papillomavirus type 58 DNA sequence.  
A/Reference number: A36779; MUID:92024102; PMID:1656594  
A/Accession: E36779  
A/Status: translation not shown  
A/Molecule type: DNA  
A/Residues: 1-149 <KIR>  
A/Cross-references: UNIPROT:P26555; GB:D90400; NID:g222386; PIDN:EAA31845.1; PID:g3337090  
C/Superfamily: papillomavirus E6 protein  
C/Keywords: DNA binding; early protein; zinc finger  
F:30-66/Region: zinc finger CCCC motif  
F:103-139/Region: zinc finger CCCC motif

Query Match 50.0%; Score 60; DB 1; Length 149;  
Best Local Similarity 52.4%; Pred.No. 0.072;  
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 CIDFGSRIRELRHYSVSYGD 22  
| : | : | : | : | : | :  
Db 66 CLRLLSKISEYRHNYS-VYGD 86

## RESULT 12

E6 protein - human papillomavirus type 52  
A:Accession: A61237  
C:Species: human papillomavirus type 52  
C:Date: 12-May-1994 #sequence\_revision 12-May-1994 #text\_change 03-May-1996  
C:Accession: A61237  
R;Takami, Y.; Kondoh, G.; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, A.; Warsa, U.  
Int. J. Cancer 48, 516-522, 1991  
A:Title: Cloning and characterization of human papillomavirus type 52 from cervical carcinoma  
A:Reference number: A61237; PMID:91258022; PMID:1646174  
A:Accession: A61237  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-148 <RAK>  
C:Superfamily: papillomavirus E6 protein

Query Match 49.2%; Score 59; DB 2; Length 148;

Best Local Similarity 55.0%; Pred. No. 0.1;

Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 CIDFGSRIRLRYHSDSVYG 21

:|:|:|:|:|:|:|:|:|

Db 66 CLFSLKISEYRHYQYSLYG 85

## RESULT 13

E6 protein - human papillomavirus type 34  
A:Accession: S36515  
C:Species: human papillomavirus type 34  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S36515  
R;Dellius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36515

A:Molecule type: DNA

A:Residues: 1-148 <DEL>

A:Cross-references: UNIPROT:P36811; EMBL:X74476; NID:g396989; PIDN:CAA52555.1; PID:g3969

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match

Best Local Similarity 50.0%; Pred. No. 0.1;

Matches 10; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 2 CIDFGSRIRLRYHSDSVYG 21

:|:|:|:|:|:|:|:|:|

Db 67 CLFYSKVRQYRRYNOSVYG 86

## RESULT 14

E6 protein - human papillomavirus type 52  
A:Accession: S36573  
C:Species: human papillomavirus type 52  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S36573  
R;Dellius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36573

A:Molecule type: DNA

A:Residues: 1-148 <DEL>

A:Cross-references: UNIPROT:P36814; EMBL:X74481; NID:g397038; PIDN:CAA52585.1; PID:g3970

C:Superfamily: papillomavirus E6 protein

C:Keywords: DNA binding; early protein; nucleus; zinc finger

Query Match

Best Local Similarity 55.0%; Pred. No. 0.1;

Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 2 CIDFGSRIRLRYHSDSVYG 21

:|:|:|:|:|:|:|:|:|

Db 66 CLFSLKISEYRHYQYSLYG 85

## RESULT 15

E6 protein - human papillomavirus type 26  
A:Accession: S36544  
C:Species: human papillomavirus type 26  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S36544  
R;Dellius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36544

A:Molecule type: DNA

A:Residues: 1-150 <DEL>

A:Cross-references: UNIPROT:P36807; EMBL:X74472; NID:g396956; PIDN:CAA52530.1; PID:g3969

C:Superfamily: papillomavirus E6 protein

C:Keywords: early protein; zinc finger

Query Match

Best Local Similarity 52.4%; Pred. No. 0.15;

Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 KCIDFGSRIRLRYHSDSVYG 21

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Db 65 RCVIFYSKITEYRRTCSVYG 85

Search completed: November 22, 2004, 20:32:42

Job time : 23.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 22, 2004, 20:32:01 ; Search time 97.5 Seconds  
(without alignments)  
79.906 Million cell updates/sec

Title: US-10-612-818-5

Perfect score: 120

Sequence: 1 KCIDFGSRIELRHYSVYGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	120	100.0	22	16	US-10-612-818-5
2	111	92.5	172	16	US-10-472-724-6
3	111	92.5	278	13	US-10-000-903-21
4	111	92.5	383	13	US-10-000-903-23
5	68	56.7	151	14	US-10-177-390-6
6	65	54.2	171	16	US-10-472-724-2
7	65	54.2	266	9	US-09-367-309A-1
8	65	54.2	273	13	US-10-000-903-4
9	65	54.2	292	13	US-10-000-903-10
10	65	54.2	371	13	US-10-000-903-6
11	65	54.2	390	13	US-10-000-903-14
12	50	41.7	20	16	US-10-476-570-12
13	49	40.8	936	14	US-10-369-493-5053

Sequence 3, Appli  
Sequence 102875,  
Sequence 3356, Ap  
Sequence 32, Appl  
Sequence 191497,  
Sequence 39, Appl  
Sequence 41, Appl  
Sequence 42, Appl  
Sequence 40, Appl  
Sequence 275384,  
Sequence 174143,  
Sequence 282891,  
Sequence 282892,  
Sequence 282893,  
Sequence 489, App  
Sequence 6142, Ap  
Sequence 3115, Ap  
Sequence 48, Appl  
Sequence 49, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 10, Appl  
Sequence 9, Appl  
Sequence 11, Appl  
Sequence 13, Appl  
Sequence 47, Appl  
Sequence 2286, Ap  
Sequence 45, Appl  
Sequence 216980,  
Sequence 204, App  
Sequence 205, App

9 US-09-220-091-3  
605 16 US-10-437-963-102875  
1462 15 US-10-320-797-3356  
15 16 US-10-476-570-32  
397 16 US-10-437-963-191497  
187 14 US-10-140-293-39  
187 14 US-10-140-293-41  
187 14 US-10-140-293-42  
189 14 US-10-140-293-40  
794 17 US-10-425-115-275384  
182 15 US-10-424-599-174143  
198 15 US-10-424-599-282891  
208 15 US-10-424-599-282892  
324 15 US-10-424-599-282893  
506 14 US-10-310-154-489  
512 9 US-09-738-636-6142  
890 14 US-10-389-493-3115  
1048 15 US-10-016-248-48  
1274 15 US-10-016-248-49  
1783 14 US-10-467-042-11  
1800 14 US-10-276-934-12  
1826 14 US-10-276-934-10  
2008 14 US-10-276-934-11  
2306 14 US-10-276-934-14  
2352 14 US-10-276-934-13  
3389 15 US-10-016-248-47  
3389 16 US-10-408-765A-2286  
3508 15 US-10-016-248-46  
372 15 US-10-424-599-216980  
509 15 US-10-074-978A-204  
509 15 US-10-074-978A-205

#### ALIGNMENTS

#### RESULT 1

US-10-612-818-5  
; Sequence 5, Application US/10612818  
; Publication No. US20040110925A1  
; GENERAL INFORMATION:  
; APPLICANT: Impact Diagnostics  
; APPLICANT: Impact Diagnostics  
; TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruses  
; TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papil  
; TITLE OF INVENTION: Associated Cancers  
; FILE REFERENCE: 3352-2-2  
; CURRENT APPLICATION NUMBER: US/10/612,818  
; CURRENT FILING DATE: 2003-07-01  
; PRIOR APPLICATION NUMBER: US 60/394,172  
; PRIOR FILING DATE: 2002-07-02  
; PRIOR APPLICATION NUMBER: US 09/828,645  
; PRIOR FILING DATE: 2001-04-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 22  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Derived from the E6 early coding region of HPV 18  
US-10-612-818-5

Query Match 100.0%; Score 120; DB 16; Length 22;  
Best Local Similarity 100.0%; Pred.No.1.6e-11;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KCIDFGSRIELRHYSVYGD 22

Db 1 KCIDFGSRIELRHYSVYGD 22

```

; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-903-23

Query Match          92.5%; Score 111; DB 13; Length 383;
Best Local Similarity 95.5%; Pred. No. 8.9e-09;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 KCIDFGSRIRLEHYSDSYGD 22
Db      178 KCIDFYRIRLEHYSDSYGD 199
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        |||.....|||

RESULT 5
US-10-177-390-6
; Sequence 6, Application US/10177390
; Publication No. US20030143743A1
; GENERAL INFORMATION:
; APPLICANT: Schuler, Gerold
; APPLICANT: N.V. Antwerps Innovatiecentrum
; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with Linear
; TITLE OF INVENTION: Polynucleotides by Electroporation
; FILE REFERENCE: 021505wo/JH/ml
; CURRENT APPLICATION NUMBER: US/10/177,390
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-177-390-6

Query Match          56.7%; Score 68; DB 14; Length 151;
Best Local Similarity 61.9%; Pred. No. 0.016;
Matches 13; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 KCIDFGSRIRLEHYSDSYVG 21
Db      65 KCLKFYKISEYRHYSYVG 85
        |||.||..|||
        |||.||..|||

RESULT 6
US-10-472-724-2
; Sequence 2, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22

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; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 171
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-472-724-2

Query Match          54.2%; Score 65; DB 16; Length 171;
Best Local Similarity 57.1%; Pred. No. 0.054;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLRYHSDSVYG 21
Db 77 KCLKFYSKISEYRHYCYSLYG 97

RESULT 7
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Publication No. US20020081329A1
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JTM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; CURRENT APPLICATION NUMBER: US/09/367,309A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

Query Match          54.2%; Score 65; DB 9; Length 266;
Best Local Similarity 57.1%; Pred. No. 0.087;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLRYHSDSVYG 21
Db 72 KCLKFYSKISEYRHYCYSLYG 92

RESULT 8
US-10-000-903-4
; Sequence 4, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match          54.2%; Score 65; DB 13; Length 273;
Best Local Similarity 57.1%; Pred. No. 0.09;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLRYHSDSVYG 21
Db 178 KCLKFYSKISEYRHYCYSLYG 198

RESULT 9
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match          54.2%; Score 65; DB 13; Length 292;
Best Local Similarity 57.1%; Pred. No. 0.096;
Matches 12; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRLRYHSDSVYG 21
Db 197 KCLKFYSKISEYRHYCYSLYG 217

RESULT 10
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6
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Qy 2 CIDFGSRIRLRYSDSVY 20  
 Db 349 CTQFGGSVLDARHPSDHTF 367

RESULT 15

US-10-437-963-102875  
 ; Sequence 102875, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barzduk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 102875  
 ; LENGTH: 605  
 ; TYPE: PRT  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_100359C.1.pap  
 US-10-437-963-102875

Query Match 40.0%; Score 48; DB 16; Length 605;  
 Best Local Similarity 33.3%; Pred.No. 95;  
 Matches 7; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 CIDFGSRIRLRYSDSVYGD 22  
 Db 372 CVERGQRLVYKHPSETLDD 392

Search completed: November 22, 2004, 20:48:54  
 Job time : 97.5 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2004, 20:18:17 ; Search time 127.5 Seconds  
(without alignments)  
99.280 Million cell updates/sec

Title: US-10-612-818-5

Sequence: 1 KCIDFGSRIEELRHYSVYGD 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	111	92.5	158	1	VE6_HPV18
2	111	92.5	158	2	Q9NPF8
3	111	92.5	158	2	AAP20594
4	96	80.0	158	1	VE6_HPV45
5	96	80.0	158	2	Q9Y474
6	96	80.0	158	2	O10608
7	86	71.7	160	2	Q81984
8	82	68.3	157	2	Q9WHG0
9	81	67.5	158	1	VE6_HPV70
10	75	62.5	158	1	VE6_HPV39
11	73	60.8	151	2	Q9IR59
12	73	60.8	151	2	Q994A0
13	71	59.2	158	1	VE6_HPV68
14	71	59.2	158	1	VE6_HPVME
15	71	59.2	158	2	Q7KYX8
16	71	59.2	158	2	CAA74931
17	71	59.2	162	2	Q9UI29
18	68	56.7	84	2	Q80882
19	68	56.7	130	2	Q919B8
20	68	56.7	130	2	Q919C0
21	68	56.7	130	2	Q919C2
22	68	56.7	130	2	Q919C8
23	68	56.7	138	2	Q919D2
24	68	56.7	143	2	Q919C4
25	68	56.7	151	2	O12335
26	68	56.7	151	2	O77JC7
27	68	56.7	151	2	Q77ZJ5
28	68	56.7	151	2	Q80963
29	68	56.7	151	2	Q99648
30	68	56.7	151	2	Q89852
31	68	56.7	151	2	Q8BB19

32	68	56.7	151	2	Q8BB20	Q8bb20 human papil
33	68	56.7	151	2	Q9WMP5	Q9wmp5 human papil
34	68	56.7	158	2	Q7IB17	Q7ib17 human papil
35	68	56.7	158	2	Q9WH13	Q9wh13 human papil
36	68	56.7	158	2	Q9QDH5	Q9qdh5 human papil
37	68	56.7	158	2	AAQ10712	AAQ10712 human pap
38	65	54.2	90	2	Q80884	Q80884 human papil
39	65	54.2	99	2	Q919B2	Q919b2 human papil
40	65	54.2	103	2	Q919D6	Q919d6 human papil
41	65	54.2	130	2	Q919B4	Q919b4 human papil
42	65	54.2	130	2	Q919D0	Q919d0 human papil
43	65	54.2	143	2	Q919B6	Q919b6 human papil
44	65	54.2	151	1	VE6_HPV51	P26554 human papil
45	65	54.2	151	2	O12336	O12336 human papil

#### ALIGNMENTS

RESULT 1  
VE6\_HPV18  
ID\_VE6\_HPV18 STANDARD; PRT; 158 AA.  
AC P06463;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE E6 protein.  
GN Names=E6,  
OS Human papillomavirus type 18.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10582;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87283982; PubMed=3039146;  
RA Cole S.T., Danos O.;  
RT "Nucleotide sequence and comparative analysis of the human  
papillomavirus type 18 genome. Phylogeny of papillomaviruses and  
repeated structure of the E6 and E7 gene products.";  
J. Mol. Biol. 193:599-608(1987).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=86306665; PubMed=3018129;  
RA Matlashewski G., Banks L., Wu-Liao J., Spence P., Pim D., Crawford L.;  
RT "The expression of human papillomavirus type 18 E6 protein in bacteria  
and the production of anti-E6 antibodies.";  
J. Gen. Virol. 67:1909-1916(1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88188247; PubMed=2933614;  
RA Inagaki Y., Tsunokawa Y., Takebe N., Nawa H., Nakanishi S., Terada M.,  
Sugimura T.;  
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18  
transcripts in HeLa cells.";  
J. Virol. 62:1640-1646(1988).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87053870; PubMed=3023067;  
RA Schneider-Gaedcke A., Schwarz E.;  
RT "Different human cervical carcinoma cell lines show similar  
transcription patterns of human papillomavirus type 18 early genes.";  
EMBO J. 5:2285-2292(1986).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=87218459; PubMed=3034571;  
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;  
RT "Identification of early proteins of the human papilloma viruses type  
16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";  
EMBO J. 6:139-144(1987).  
RN [6]  
RP ZINC-BINDING.  
RX MEDLINE=89385606; PubMed=2550872;  
RA Grossman S.R., Laimins L.A.;

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DR InterPro; IPR001334; E6.  
Pfam; PF00518; E6; 1.  
SQ SEQUENCE 158 AA; 18896 MW; 5BCF13CF43D407AF CRC64;  
  
Query Match          92.5%; Score 111; DB 2; Length 158;  
Best Local Similarity 95.5%; Pred.No. 7e-09; Indels  
Matches 21; Conservative 0; Mismatches 1; Gaps 0;  
  
QY      1 KCIDFGSRIRELRHYSDSVYGD 22  
Db       |||||  
         KCIDFYSRIRELRHYSDSVYGD 88  
  
RESULT 3  
AAP20594 PRELIMINARY; PRT; 158 AA.  
ID AAP20594  
AC AAP20594  
DT 02-VAR-2004 (TrEMBLrel. 27, Created)  
DT 02-VAR-2004 (TrEMBLrel. 27, Last sequence update)  
DE 02-VAR-2004 (TrEMBLrel. 27, Last annotation update)  
E6 Protein.  
OS Human papillomavirus type 18.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
NCBI_TaxID=10582;  
CX [1]  
RN RN  
RP SEQUENCE FROM N.A.  
RA Chen Z., Burk R.D.;  
RT "The newly modified full genome sequence of HPV18 prototype (Cole,  
RL 1987), with E6, E7, E1, E2, E4, E5, E2 and L1 ORFs.";  
R Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AY262282; AAP20594.1; -.  
SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D157FA CRC64;  
  
Query Match          92.5%; Score 111; DB 2; Length 158;  
Best Local Similarity 95.5%; Pred.No. 7e-09; Indels  
Matches 21; Conservative 0; Mismatches 1; Gaps 0;  
  
QY      1 KCIDFGSRIRELRHYSDSVYGD 22  
Db       |||||  
         KCIDFYSRIRELRHYSDSVYGD 88  
  
RESULT 4  
VE6_HPV45:  
ID VE6_HP45 STANDARD; PRT; 158 AA.  
AC AC  
DT 01-MAY-1991 (Rel. 18, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
E6 protein.  
GN Name=E6;  
OS Human papillomavirus type 45.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
NCBI_TaxID=10593;  
CX [1]  
RN RN  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94265501; PubMed=8205838;  
RA Delius H., Hofmann B.;  
RT "primer-directed sequencing of human papillomavirus types.";  
RL Curt. Top. Microbiol. Immunol. 186:13-31(1994).  
[2]  
RN RN  
RP SEQUENCE FROM N.A.  
RA Kaplan J.B., Burk R.D.;  
RL Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.  
CC -!- FUNCTION: This protein has transforming activity in vitro.  
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double  
CC stranded DNA (in vitro).  
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.  
-----  
CC  
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```



AC  
 010608;  
 DT  
 01-JUL-1997 (TRENDELrel. 04, Created)

ID Q9WHEG0 PRELIMINARY; FRI; 15 / AA.



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RESULT 11
Q91R59 PRELIMINARY; PRT; 151 AA.
ID Q91R59
AC Q91R59;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE E6 protein.
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=129724;
RN [1]
RP MEDLINE=20087399; PubMed=10618284;
RA Kino N., Sato T., Sato Y., Sugase M., Matsukura T.;
RT "Molecular cloning and nucleotide sequence analysis of a novel human
RT papillomavirus (Type 82) associated with vaginal intraepithelial
RT neoplasia."
RL Clin. Diagn. Lab. Immunol. 7:91-95(2000).
DR EMBL; AB027021; BAA90735.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR ZN_FING 105 141
SQ SEQUENCE 151 AA; 18006 MW; 949358742A0375B5 CRC64;

Query Match 60.8%; Score 73; DB 2; Length 151;
Best Local Similarity 71.4%; Pred. No. 0.0047;
Matches 15; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSVYVG 21
|||:|||||:|||||
Db 65 KCLMFYSRIRRYRSVYVG 85

RESULT 12
Q994A0 PRELIMINARY; PRT; 151 AA.
ID Q994A0
AC Q994A0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative transforming protein E6.
OS Human papillomavirus type 82.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=129724;
RN [1]
RP SEQUENCE FROM N.A.
RA Terai M., Burk R.D.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF293961; AAK28449.1; -.
DR GO; GO:0042025; C:host cell nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR ZN_FING 105 141
SQ SEQUENCE 151 AA; 18071 MW; 5BDC340E467CFFED CRC64;

Query Match 60.8%; Score 73; DB 2; Length 151;
Best Local Similarity 71.4%; Pred. No. 0.0047;
Matches 15; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KCIDFGSRIRRLRHYSVYVG 21
|||:|||||:|||||
Db 65 KCLMFYSRIRRYRSVYVG 85

RESULT 13
VE6_HP68
ID VE6_HP68 STANDARD; PRT; 158 AA.
AC P54667;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type 68.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=45240;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97060129; PubMed=8904450;
RA Longuet M., Beaudenon S., Orth G.;
RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,
RT related to the potentially oncogenic HPV39."
RL J. Clin. Microbiol. 34:738-744(1996).
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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CC
CC EMBL; X67160; CAA47632.1; -.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
DR DNA-binding; Early protein; Nuclear protein; Zinc-finger.
KW ZN_FING 32 68
FT ZN_FING 105 141
FT ZN_FING 105 141
SQ SEQUENCE 158 AA; 18796 MW; 46B37939CFBA6596 CRC64;

Query Match 59.2%; Score 71; DB 1; Length 158;
Best Local Similarity 68.4%; Pred. No. 0.01;
Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CIDFGSRIRRLRHYSVY 20
|||:|||||:|||||
Db 68 CIKFYAKIRRLYISVY 86

RESULT 14
VE6_HP68
ID VE6_HP68 STANDARD; PRT; 158 AA.
AC P27562;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE E6 protein.
GN Name=E6;
OS Human papillomavirus type ME180.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91374616; PubMed=1716694;
RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
RT carcinoma cell line ME180."
RL J. Virol. 65:5564-5568(1991).
CC -!- FUNCTION: Exhibits a strong, but non specific affinity for double
CC stranded DNA (in vitro).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC
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-----  
DR EMBL; W73258; -; NOT\_ANNOTATED\_CDS.

DR FIR; C40503; W6WLP; E6.

DR InterPro; IPR001334; E6.

DR Pfam; PF00518; E6; 1.

KW DNA-binding; Early protein; Nuclear protein; Zinc-finger.

FT ZN\_FING 32 68 Potential.

FT ZN\_FING 106 141 Potential.

SQ SEQUENCE 158 AA; 18738 MW; 2B1F406B563F05FC CRC64;

Query Match 59.2%; Score 71; DB 1; Length 158;

Best Local Similarity 68.4%; Pred. No. 0.01;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CIDFGSRIRRLHYSDSVY 20

DB 68 CIKFYAKIRELRYSESIVY 86

RESULT 15

Q7KYK8

ID Q7KYK8 PRELIMINARY; PRT; 158 AA.

AC Q7KYK8;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE E6 protein.

OS Human papillomavirus type 68.

OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI\_taxid=45240;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91374616; PubMed=1716694;

RA Reuter S., Delius H., Kahn T., Hofmann B., zur Hausen H., Schwarz E.;

RT "Characterization of a novel human papillomavirus DNA in the cervical

carcinoma cell line ME180."

RL J. Virol. 65:5564-5568(1991).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=98090464; PubMed=9427755;

RA Reuter S., Bartelmann M., Vogt M., Geisen C., Napierski I., Kahn T.,

RA Delius H., Lichter P., Weitz S., Korn B., Schwarz E.;

RT "APM-1, a novel human gene, identified by aberrant cotranscription

with papillomavirus oncogenes in a cervical carcinoma cell line,

RT encodes a BTB/POZ-zinc finger protein with growth inhibitory

activity."

RL EMBO J. 17:215-222(1998).

DR EMBL; Y14591; CAA74931.1; -.

DR InterPro; IPR001334; E6.

DR Pfam; PF00518; E6; 1.

SQ SEQUENCE 158 AA; 18738 MW; 2B1F406B563F05FC CRC64;

Query Match 59.2%; Score 71; DB 2; Length 158;

Best Local Similarity 68.4%; Pred. No. 0.01;

Matches 13; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 CIDFGSRIRRLHYSDSVY 20

DB 68 CIKFYAKIRELRYSESIVY 86

Search completed: November 22, 2004, 20:31:49

Job time : 128.5 secs

protein seems to be valuable in the proper management of cervical cancers  
for specific tumor markers.

Check Tags: Female; Human; Support, Non-U.S. Gov't

\*Antibodies, Viral: AN, analysis

Cervix Neoplasms: CH, chemistry

Cervix Neoplasms: PA, pathology

\*Cervix Neoplasms: VI, virology

DNA Probes, HPV

DNA, Viral: AN, analysis

Enzyme-Linked Immunosorbent Assay

\*Oncogene Proteins, Viral: AN, analysis

\*Papillomavirus, Human: GE, genetics

Papillomavirus, Human: IM, immunology

Papovaviridae Infections: EP, epidemiology

Polymerase Chain Reaction

Radioimmunoassay

Seroepidemiologic Studies

\*Tumor Markers, Biological: AN, analysis

0 (Antibodies, Viral): 0 (DNA Probes, HPV): 0 (DNA, Viral): 0 (

E6 protein, Human papillomavirus type 18): 0 (Oncogene Proteins,

Viral): 0 (Tumor Markers, Biological)

ANSWER 3 OF 11 MEDLINE on STN

1998050245 MEDLINE

Pubmed ID: 9388862

Human papillomavirus infection and esophageal squamous cell carcinoma.

He D; Tsao S W; Bu H

Department of Anatomy, Faculty of Medicine, University of Hong Kong.

Zhonghua bing li xue za zhi Chinese Journal of Pathology, (1996 Dec) 25

(6) 351-4.

Journal code: 0005331. ISSN: 0529-5807.

China

Journal; Article; (JOURNAL ARTICLE)

Chinese

Priority Journals

199801

Entered STN: 19980129

Last Updated on STN: 19980129

Entered Medline: 19980109

Human papillomavirus (HPV) infection, especially high risk types

HPV 16 and 18, have been studied widely in cervical

cancer. However, HPV infection in esophageal cancer has not been well

defined. In the present study, immunohistochemistry, PCR and Southern

blot hybridization methods were used to detect HPV infection in

127 cases of esophageal squamous cell carcinoma. Immunohistochemistry

results indicated that the virus was detected frequently in well

differentiated carcinoma. The positive rates for BPV and HPV E6

protein were 60.6% (77/127) and 43% (54/127) respectively. Meanwhile, PCR

and Southern hybridization showed that 35.9% (37/103) of esophageal

squamous cell carcinomas have HPV DNA, which included 20.4% (21/103)

HPV 16 and 7.8% (8/103) HPV 18. Of the 103 cases, only

I had both HPV 16 and HPV 18 DNA. Our results suggest

that HPV infection is present in esophageal squamous cell carcinoma and

may play a role in its pathogenesis.

Check Tags: Human; Male

Adult

Aged, 80 and over

\*Antibodies, Viral: AN, analysis

\*Carcinoma, Squamous Cell: VI, virology

DNA, Viral: AN, analysis

English Abstract

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